

Figure 1

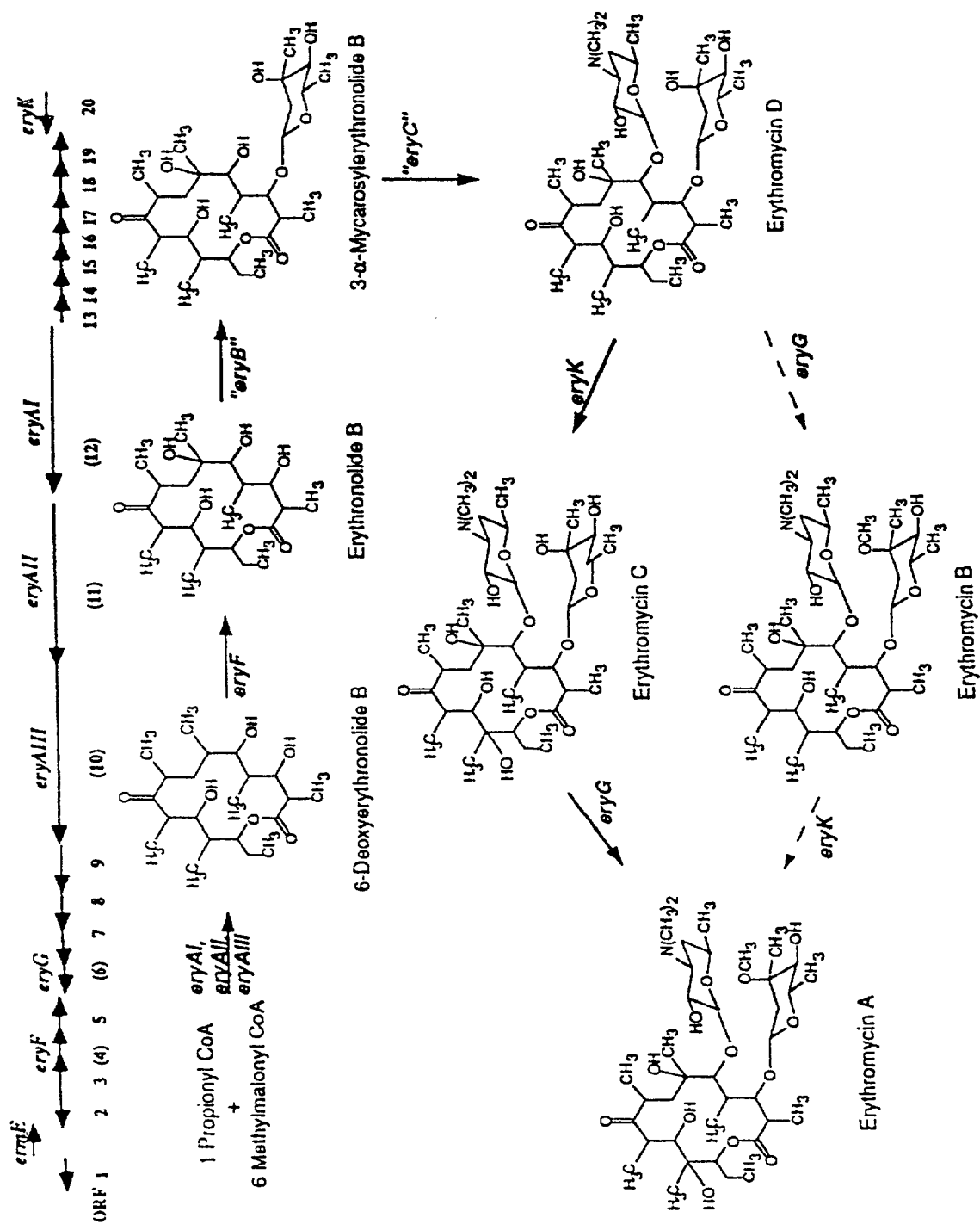


Figure 2

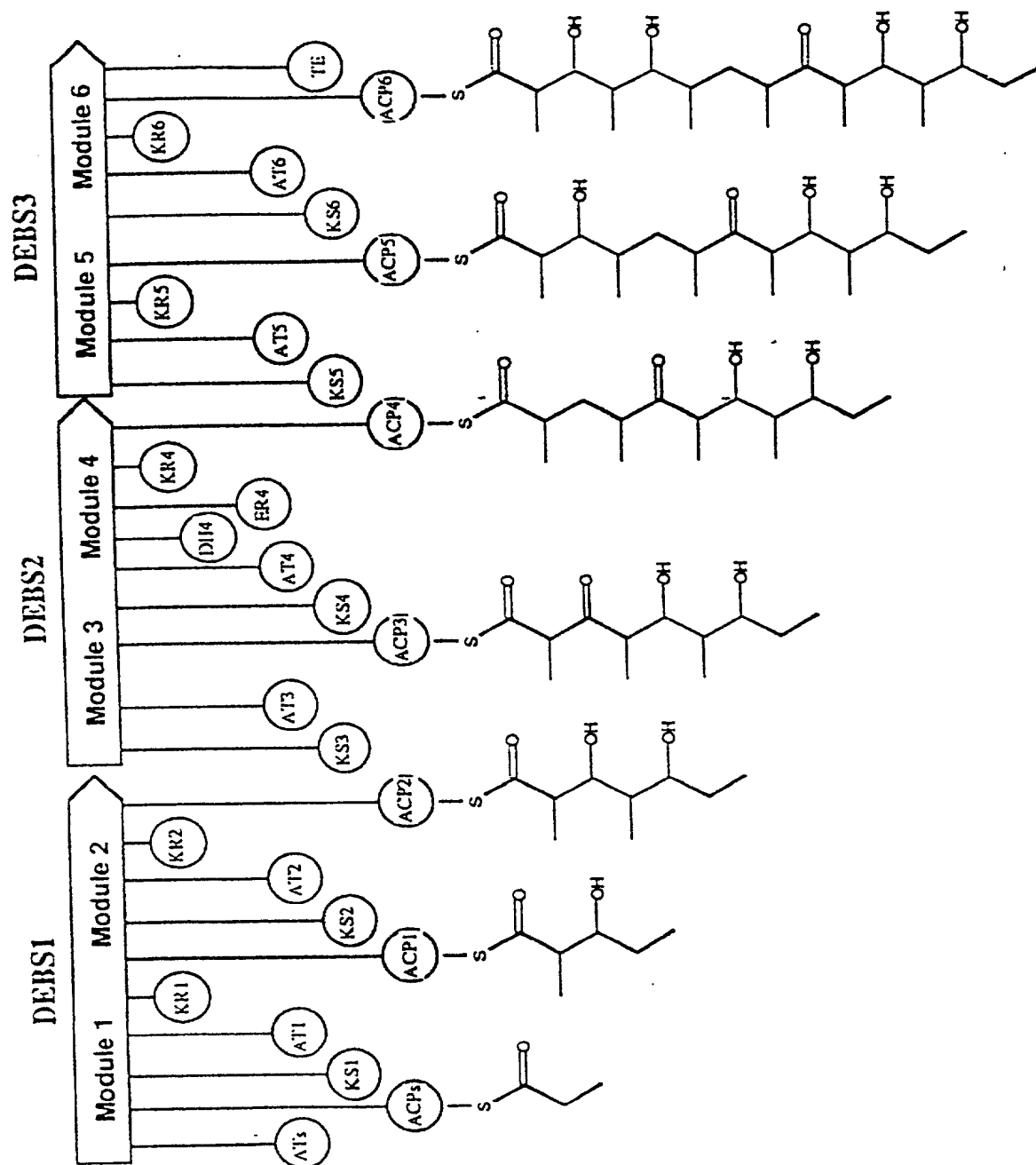


Figure 3

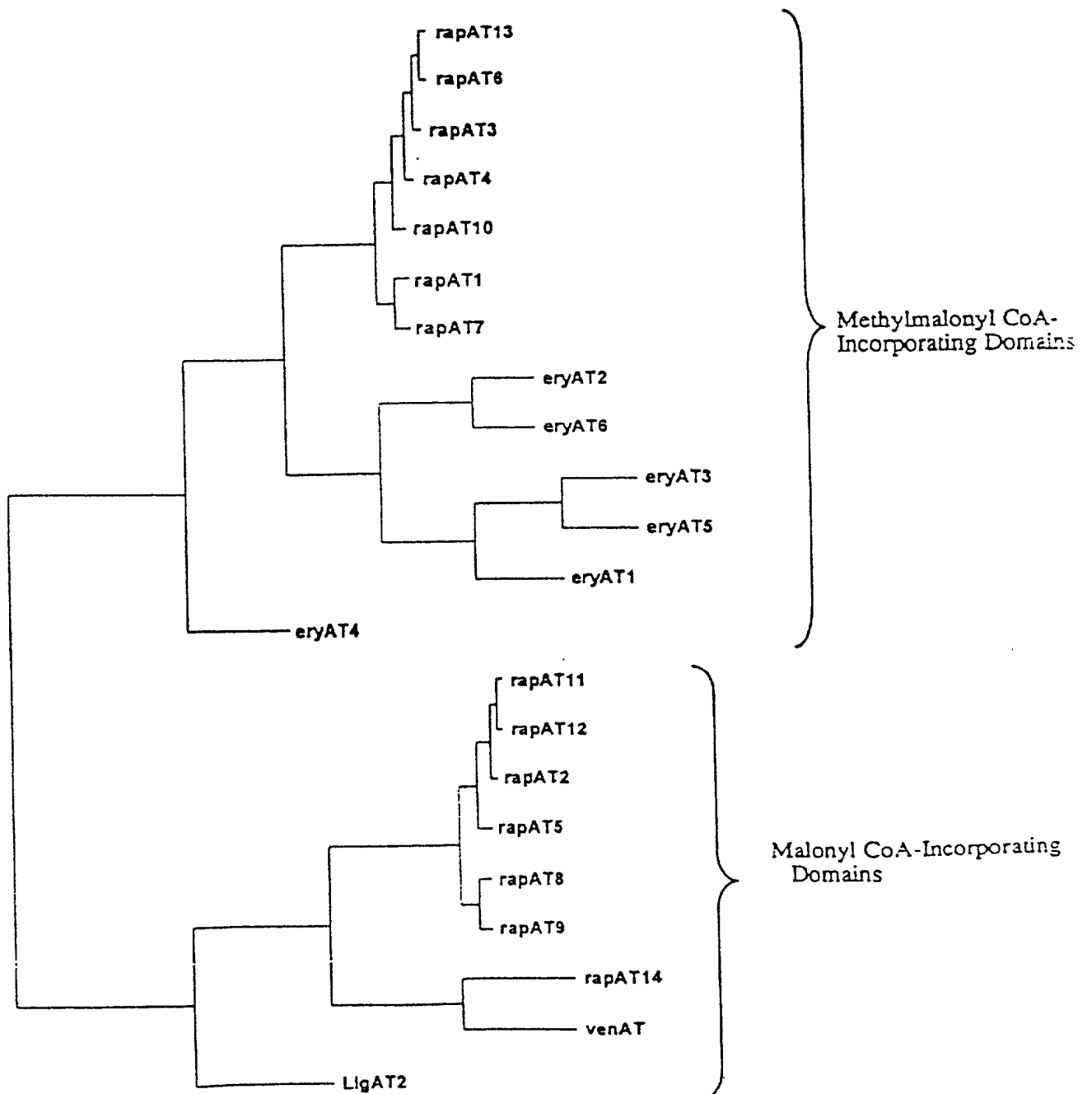
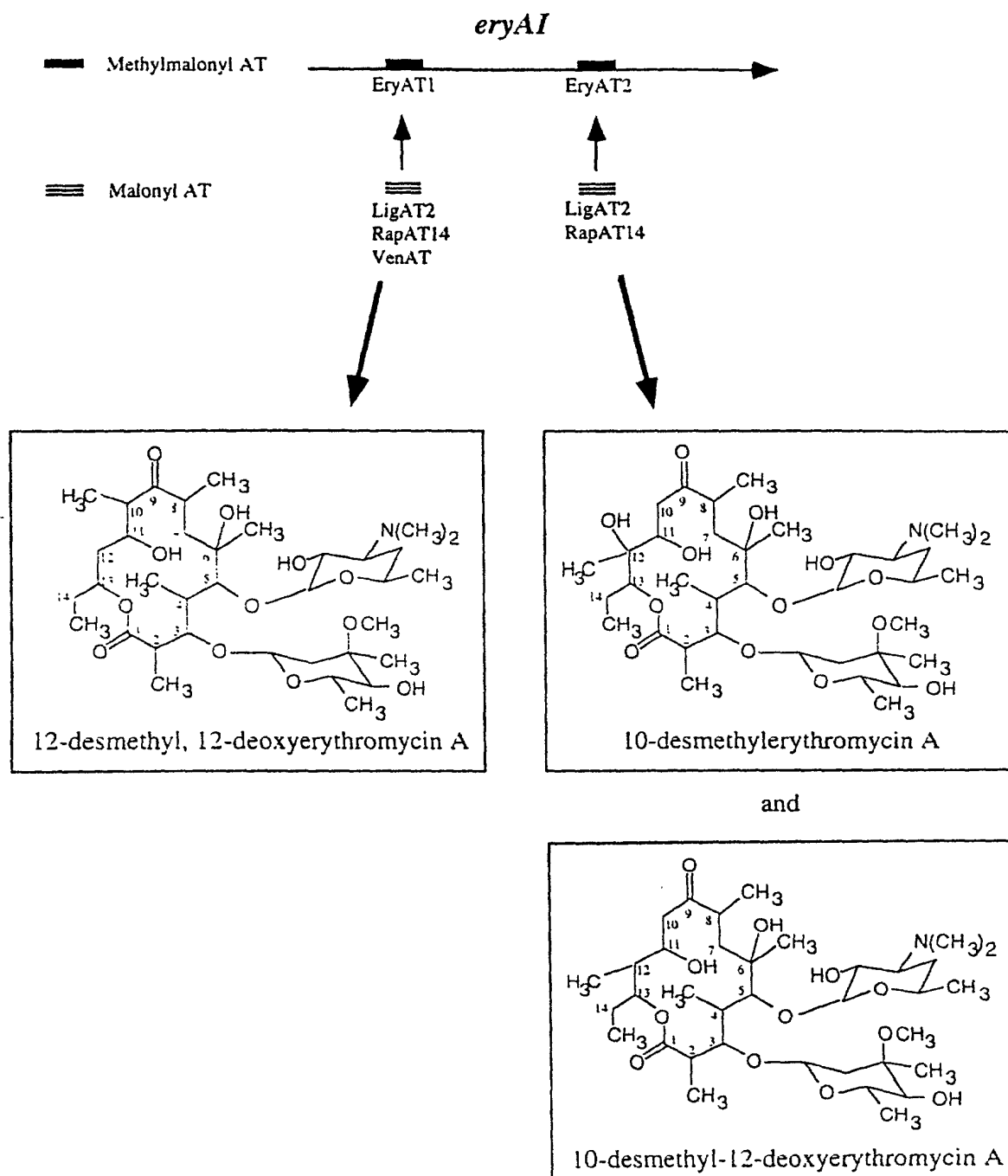


Figure 4a



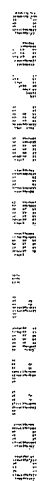
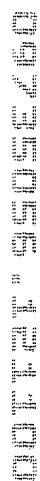
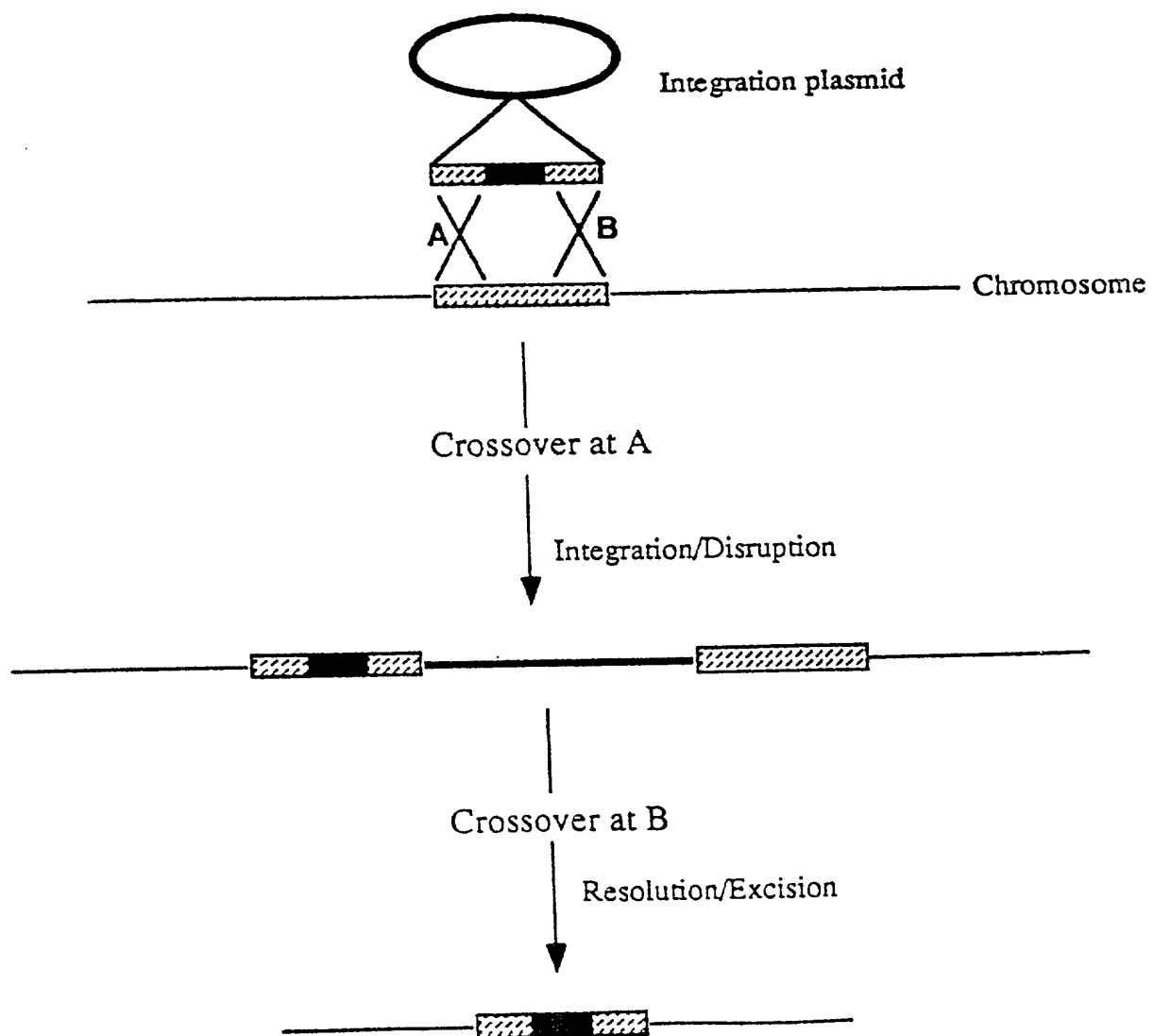
[illegible]

Figure 5



0973096-1400
00444 95038/50

Figure 6

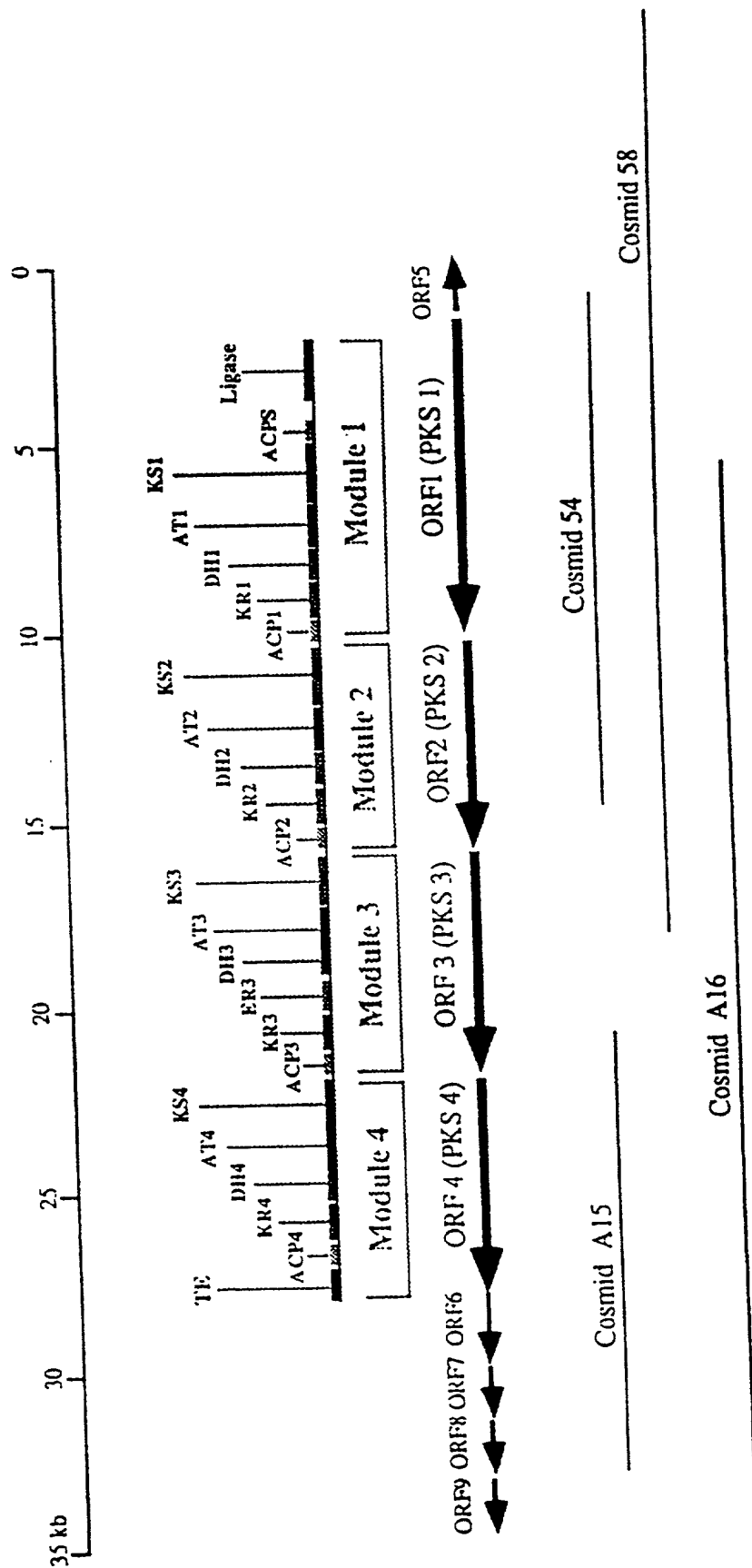


Figure 7

GGGCCGCTGGCGGTGATGTTACCGGACAGGGCTCCCAACGCCCCGGCATGGGACGACAG 60
 G P L A V M F T G Q G S Q R P G M G R Q 20
 TTGTACGAGCACTTCCCCGTCTTCGCCCAGGCACTGGACGAGGTCTTCGCACTCGCCACC 120
 L Y E H F P V F A Q A L D E V F A L A T 40
 CCGGACTACGCGAGGTGATGTTGACCCCCGACCAGGCGAAACACTCCAACGCACCGAC 180
 P G L R E V M F D P D Q A E T L Q R T D 60
 CACGCCCAGATCGCCCTGTTGCGCTTCGAAACGCCCCCTCTACCGACTCTGGGAATCCTGG 240
 H A Q I A L F A F E T A L Y R L W E S W 80
 GGCCTGCGACCCGACATGGTCTGCGGACACTCGGTGCGGAGAAATCACCGCAGCCCACGTC 300
 G L R P D M V C G H S V G E I T A A H V 100
 TCCGGCACCCCTCACCCCTCCCCGACGCGCTCCACCTCGTCACCACACGCGGCACCCCTCATG 360
 S G T L T L P D A V H L V T T R G T L M 120
 CAAAACCTGCCCCCGGCGGCGCCATGCTCGCCGTCGCCACCGACCCCCACACCCCTCCAA 420
 Q N L P P G G A M L A V A T D P H T L Q 140
 CCCCACCTCGACAACCACCACGACACCATCTCCATCGCCGCCATCAACGGCCCCCAGGCC 480
 P H L D N H H D T I S I A A I N G P H A 160
 ACCGTCTCTCCGGCGACCGCACCACCCTCCACCACATCGCCACCCAACTCAACACCAAA 540
 T V L S G D R T T L H H I A T Q L N T K 180
 ACCAACTGGCTCAACGTACGCCACGCCTTCCACTCCCCCTCATGCAACCCATCCTCCAA 600
 T N W L N V S H A F H S P L M Q P I L Q 200
 CCCTTCACCACCACCCTCAACACCCTCACCCACCACCCCCACACACACCCTCATCAGC 660
 P F T T T L N T L T H H P P H T P L I S 220
 ATGCTACCGCCACACCCACCCACCCCGACACCACCCACTGGACCCAGCACATCACCGCA 720
 M L T A T P T H P D T T H W T Q H I T A 240
 CCGTCCGCTACACCGACACCCCTCCACCACCTCCACCACCACGGCATCACACCTACCTC 780
 P V R Y T D T L H H L H H H G I T T Y L 260
 GAAATCGGCCCCGACACCACCCTCACCGCCCTCGCCCGCACCACCCTCCCCACCACCACC 840
 E I G P D T T L T A L A R T T L P T T T 280
 CACCTCATCCCCACCACCCGCGCAACCACAACGAAGTCCGCAGCACGAACGAGGCGTTG 900
 H L I P T T R R N H N E V R S T N E A L 300
 GGCAGGGTGTTCACGCTGGGCACTCGGTGGACTGGCGGGCCCTCACTCCGACCGGGAGG 960
 G R V F S V G H S V D W R A L T P T G R 320
 CGTACCTCCCTGCGACGTACCCCT 995
 R T S L P T Y P 328

00735055 "12100

Figure 8

PCR oligos:

N-terminal Oligo: 5' *Eco*RI Tag-CCTAGGCTGGCGGTGATGTTCA-3'
GGGCC

Engineered *Avr*II Homologous region

C-terminal Oligo: 5' *Bam*HI Tag-ATGCATACGTCGGCAGGGAGGTAC-3'
G GG

Engineered *Nsi*I Homologous region

PCR cloning:

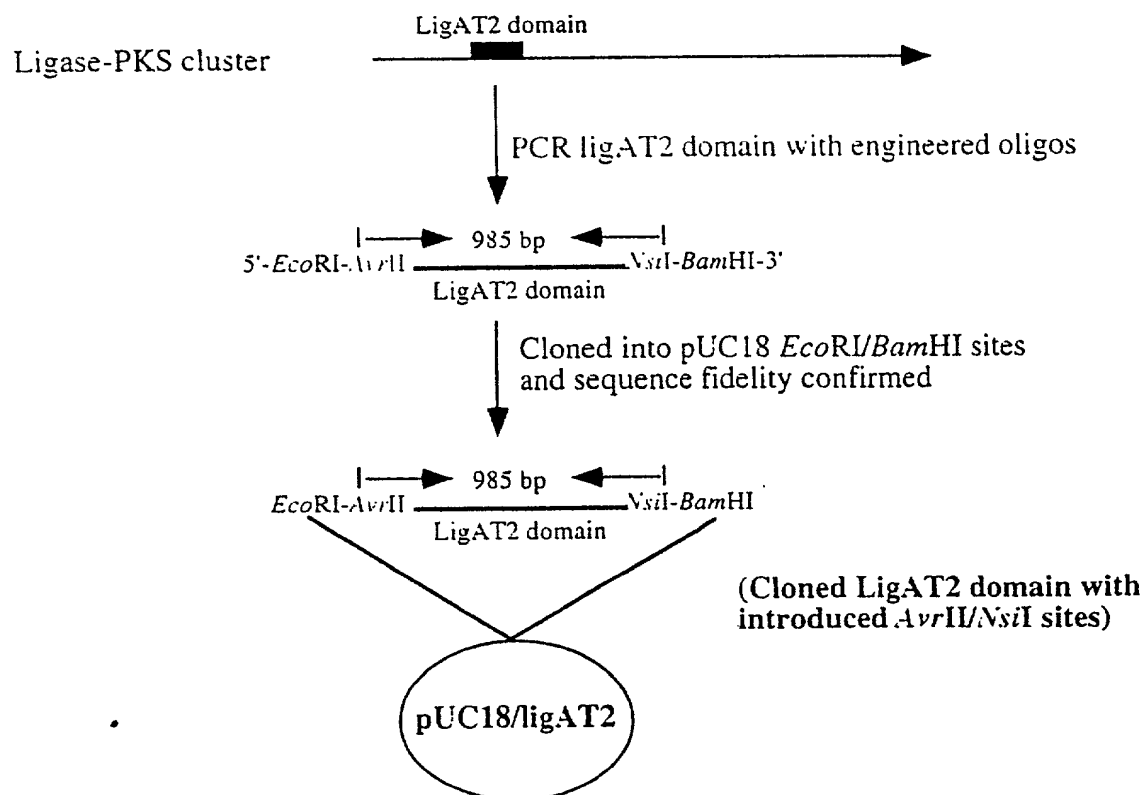


Figure 9

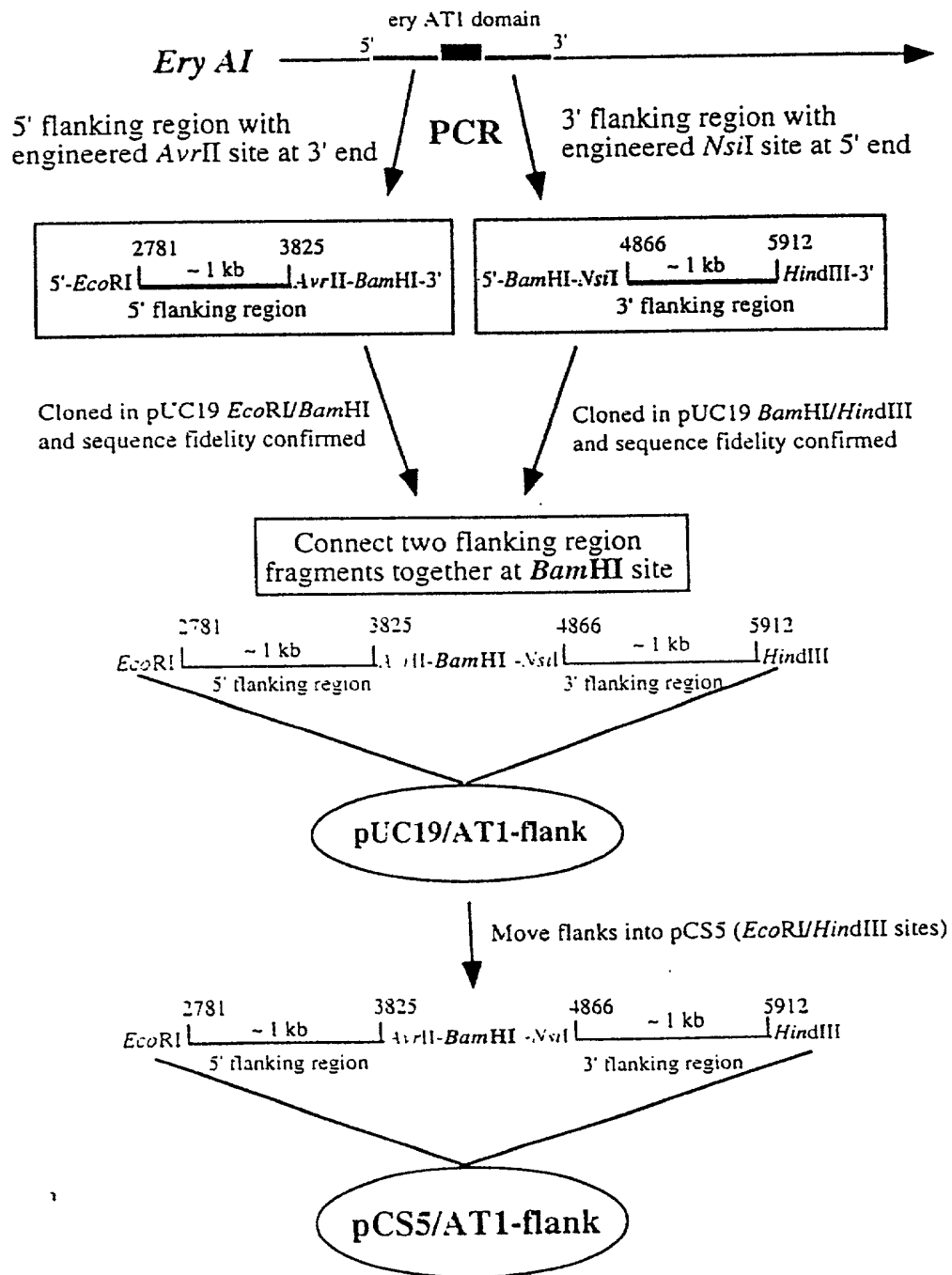


Figure 10

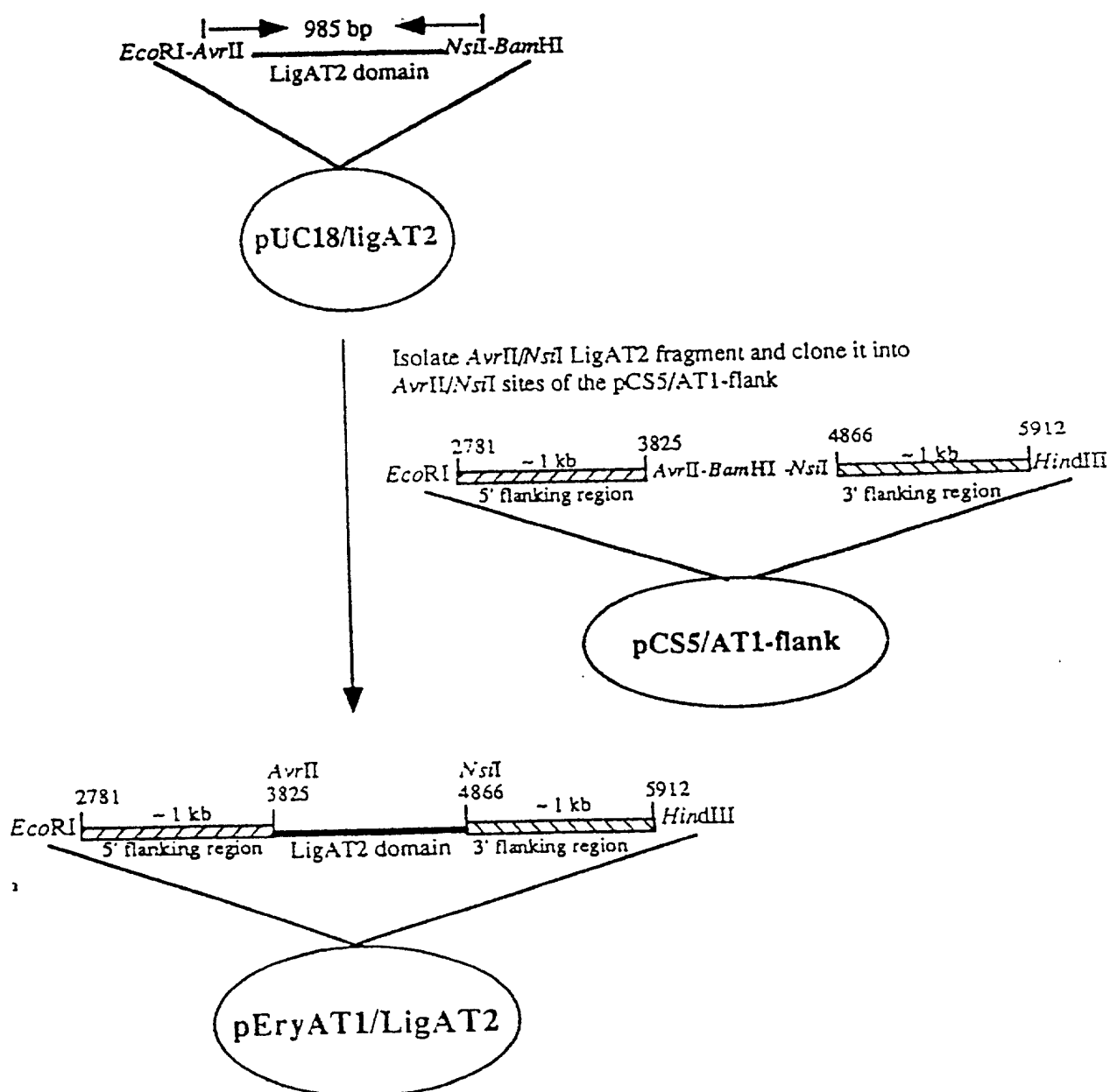


Figure 11

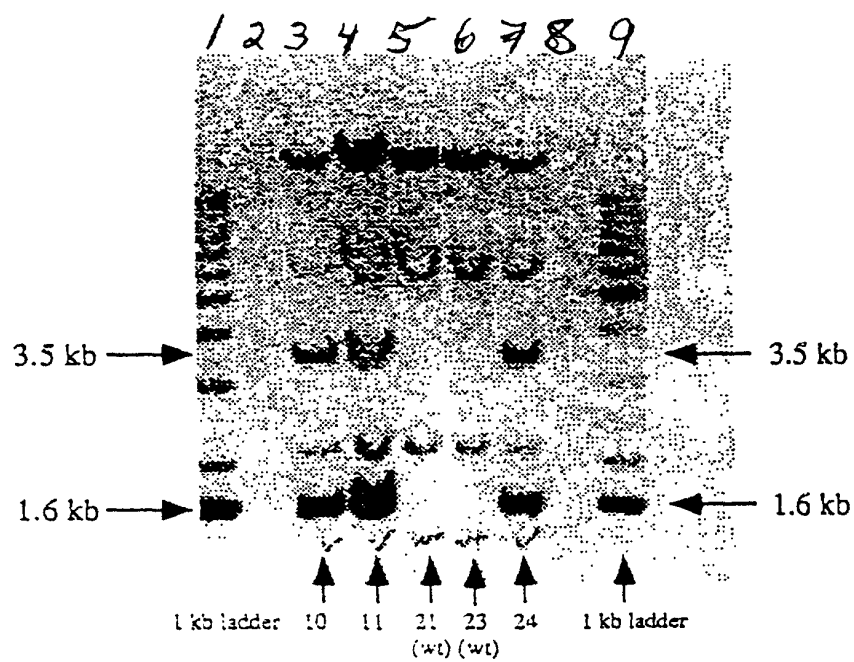


Figure 12

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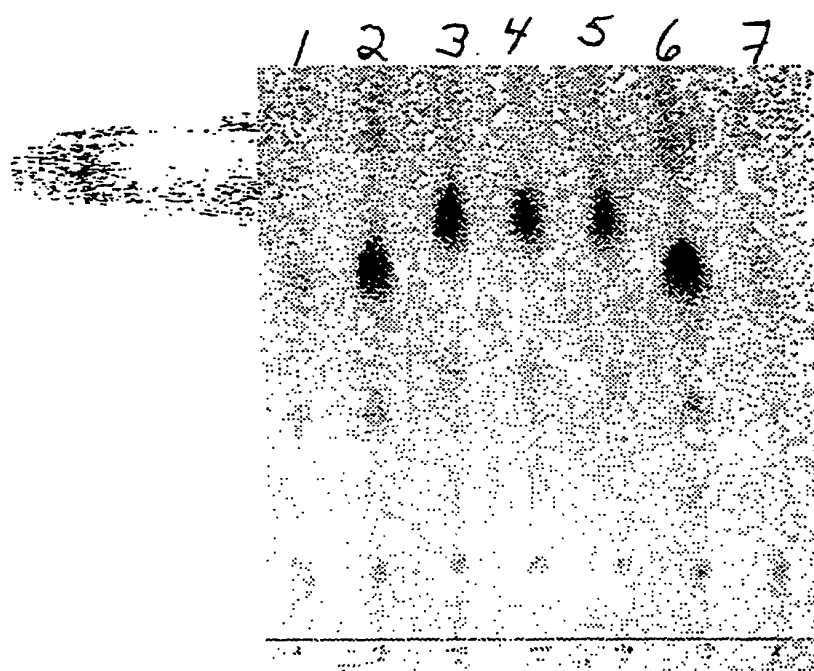


Figure 13

Construction of eryAT2 flanking regions in pCS5

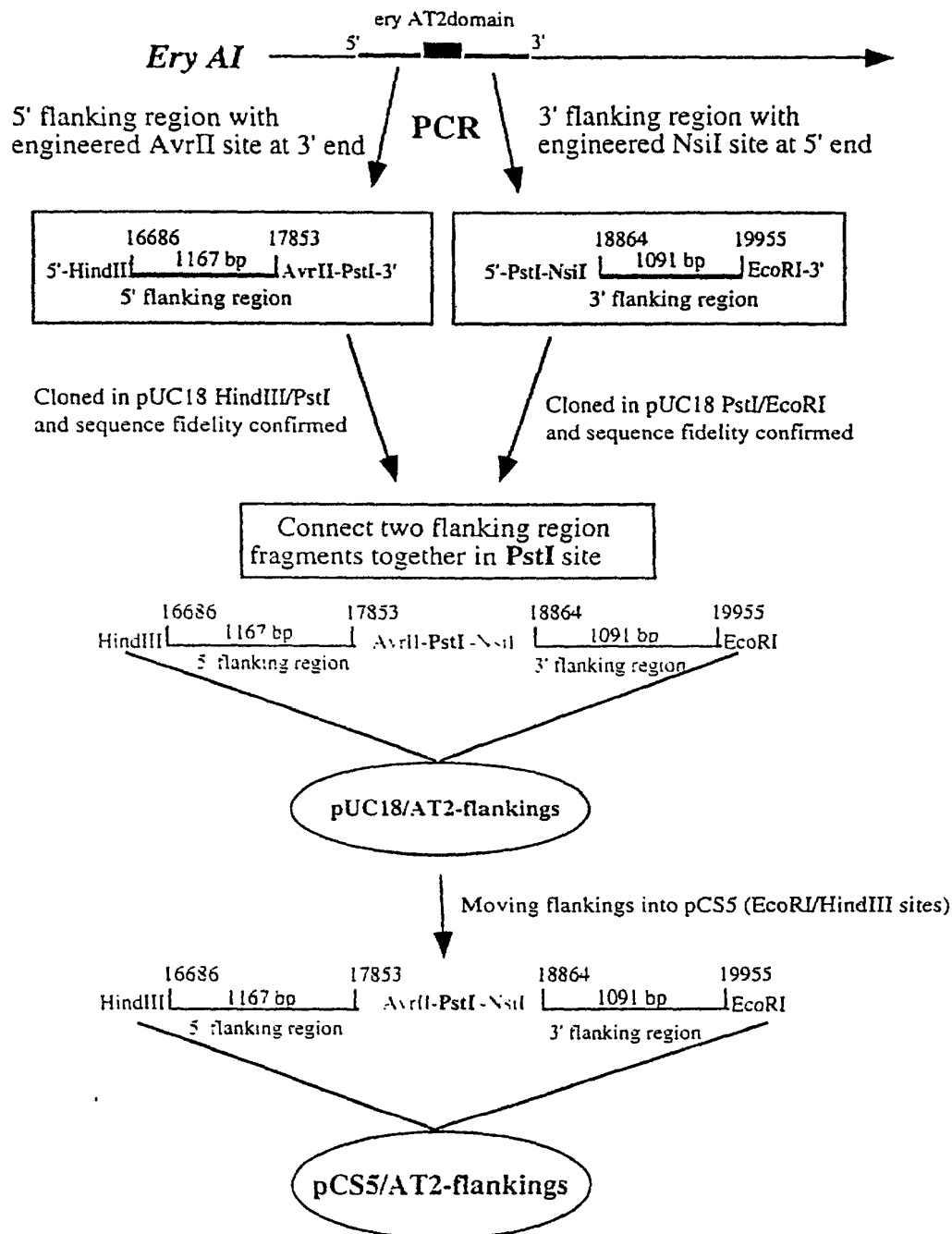


Figure 14

Scheme for Construction of pEryAT2/LigAT2 Integration Plasmid

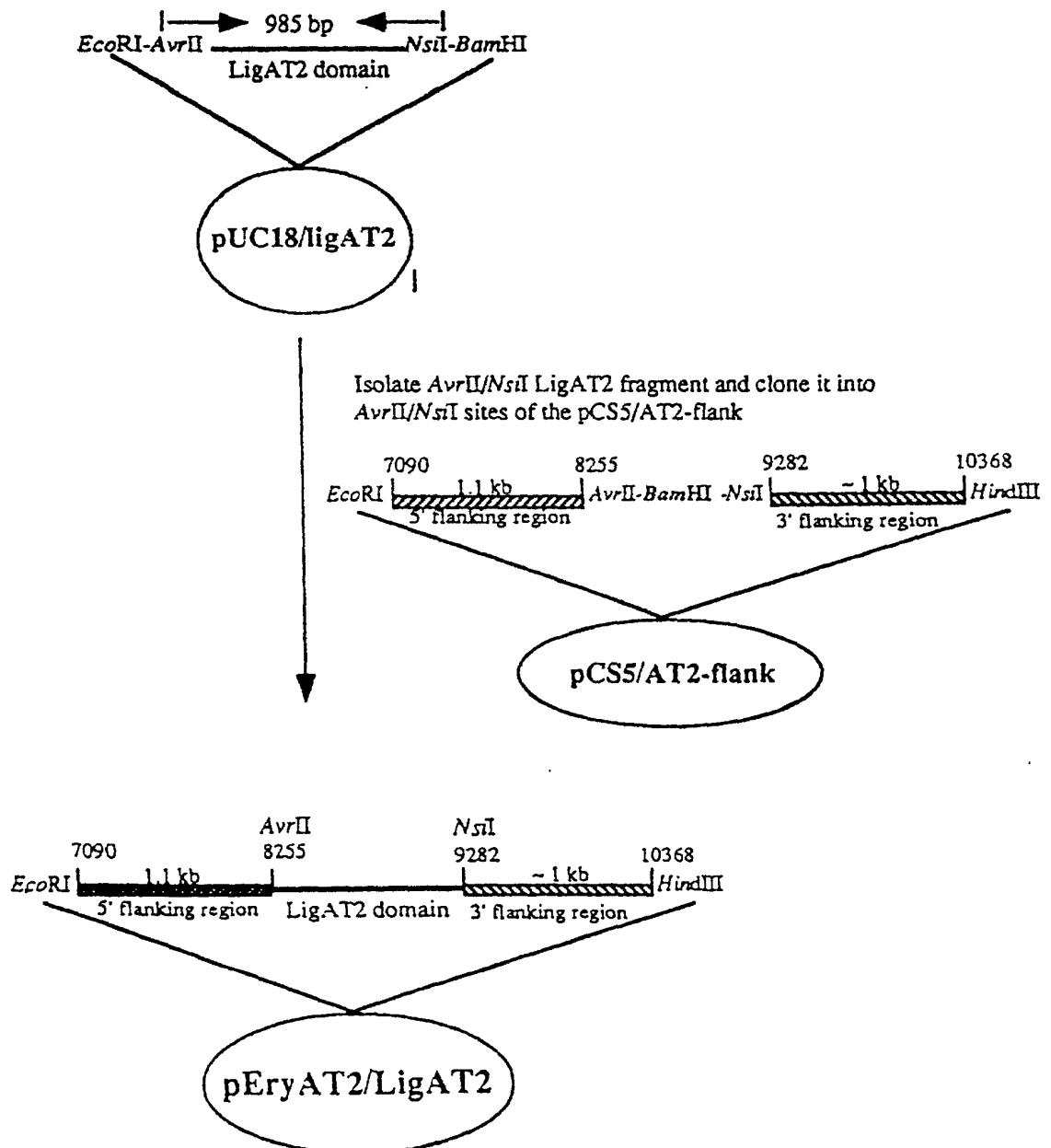


Figure 15

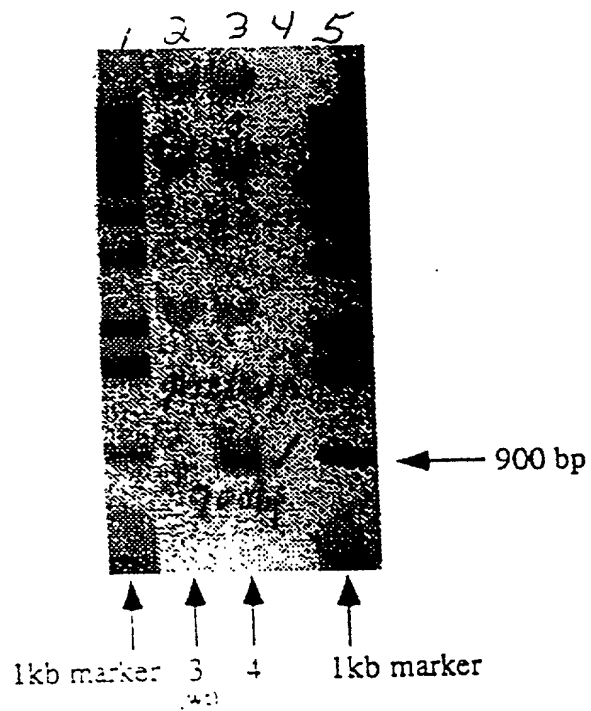
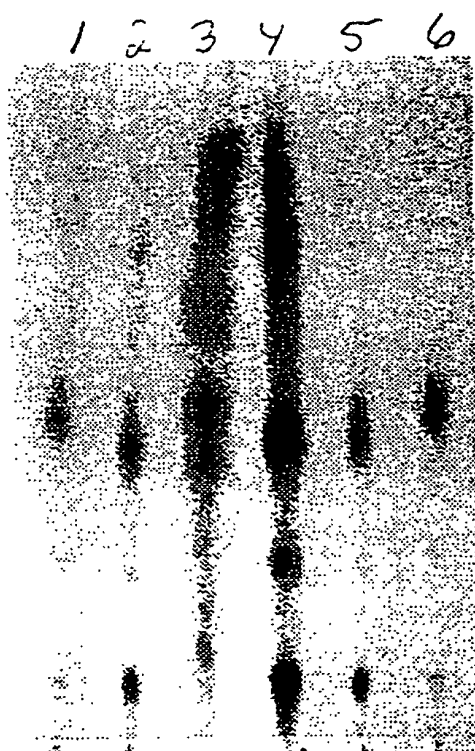


Figure 16



09735056 121100

Figure 17

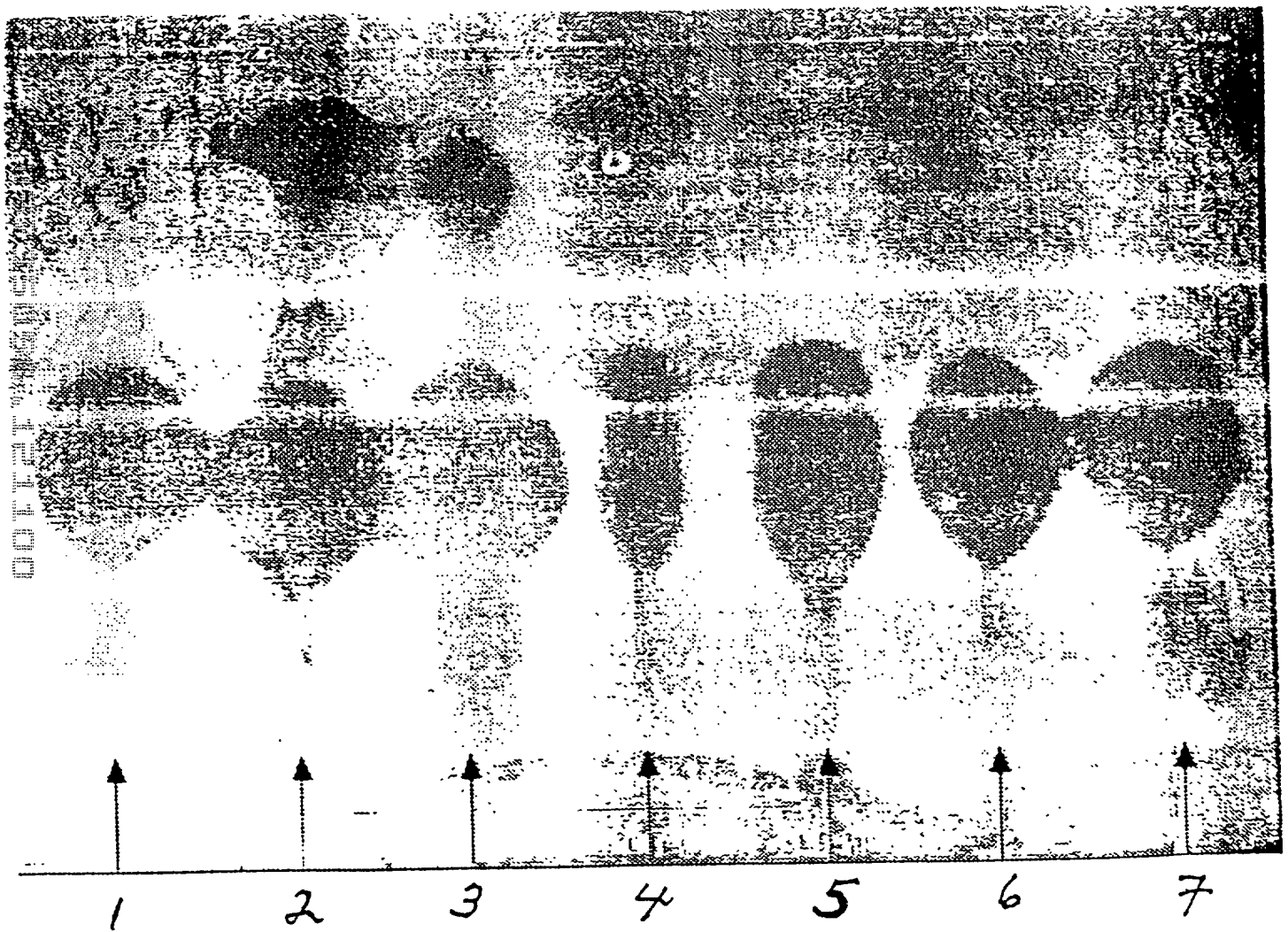


Figure 18

CCTAGGACGGCAGTCTCTGCTCACCGGGCAGGGTCTCCAGCGTCAGGGCATGGGGCGCGAA 60
 P R T A V L L T G Q G S Q R Q G M G R E 20
 CTGTACGACCGGTACCGGTGTTCCCGCCTCGTTTCGACGCGATCTGCGCTCAACTCGAC 120
 L Y D R S P V F A A S F D A I C A Q L D 40
 GGGCAACTGCCTCGTCCCCCTCAAGGACGTTCTCTTCGCCCCGAGGGGTCGGAGGACGCC 180
 G Q L P R P L K D V L F A P E G S E D A 60
 GCGCTCATCGACCGTACGGTGTTCACACAGGCGGCTCTGTTTCGCCGTGGAGACCTCCCTG 240
 A L I D R T V F T Q A A L F A V E T S L 80
 TTCCGGCTGTTTCGAGGCCCACGGCCTCGTCCCCGACTACCTCATCGGCCACTCCATCGGC 300
 F R L F E A H G L V P D Y L I G H S I G 100
 GAAGTGACCGCGGCCACCTGGCCGGGGTCTCGATCTGGCGGACGCGTGCCTCGGTC 360
 E V T A A H L A G V L D L A D A C V L V 120
 GCCCACCGCGGCCCGCTGATGCAGTCGGCCCCGGCGCGGCGCGATGGCCGCGGTCCAG 420
 A H R G R L M Q S A R A G G A M A A V Q 140
 GCGAGCGAGGACGAGGTACGCGAGGCCCTCGCGACCTTCGACGATGCGGTTGCCGTGGCC 480
 A S E D E V R E A L A T F D D A V A V A 160
 GGAGTCAACGCGCCGAACGCCACCGTCGTCTCCGGCGACGAGGACGCGGTGAGCGGGCTG 540
 G V N G P N A T V V S G D E D A V E R L 180
 GTCGCGCGCTGGCGCGAGCAGGGCAGGCGGACGAAGCGGCTGCCGGTCAGCCACGCCTTC 600
 V A R W R E Q G R R T K R L P V S H A F 200
 CACTCGCCGCACATGGACGGGATCGTCGACGAGTTCGTCACCGCCGTCTCCGGGCTCACC 660
 H S P H M D G I V D E F V T A V S G L T 220
 TTCCGCTCCCCGACGATCCCGGTCTCTCCAACGTACCGGGACCCTCGCCACCGTCGAC 720
 F R S P T I P V V S N V T G T L A T V D 240
 CAGCTGACCTCGCCCGCGTACTGGGCACGCCACATCCGCGAGGCCGTGCGCTTCGCCGAC 780
 Q L T S P A Y W A R H I R E A V R F A D 260
 GGGGTGCGGTACCTGGAGGGCGAGGGCGTCACCGAATGGCTGGAGCTCGGGCCCGACGGC 840
 G V R Y L E G E G V T E W L E L G P D G 280
 GTTCTCGTCGCCCTGGTCGAGGACTGCCTGGCGAAGGAGGCGGGATCGCTCGCGTCCGCC 900
 V L V A L V E D C L A K E A G S L A S A 300
 CTGCGCAAGGGGGCGAGCGAGCCCCACACCGTGGGCGCGGCCATGGCCCCGCGCGGTGCTG 960
 L R K G A S E P H T V G A A M A R A V L 320
 CGCGGATCCGGCCCCGACTGGGCGGCGGTGTTCCCCGGCGCACGGCGGGTCGACCTTCCG 1020
 R G S G P D W A A V F P G A R R V D L P 340
 ACGTATGCAT 1030
 T Y A 343

09735056 "121100

Figure 19

PCR oligos:

N-terminal Oligo: 5' *Eco*RI Tag- $\overbrace{\text{CCTAGGACGGCAGTCCTGCTCACC}}^{\text{AvrII}}\text{-3'}$
 GGCC
 Engineered *Avr*II | Homologous region

C-terminal Oligo: 5' *Bam*HI Tag- $\overbrace{\text{ATGCATACGTCGGAAGGTCGACCCG}}^{\text{NsiI}}\text{-3'}$
 C C
 Engineered *Nsi*I | Homologous region

PCR cloning:

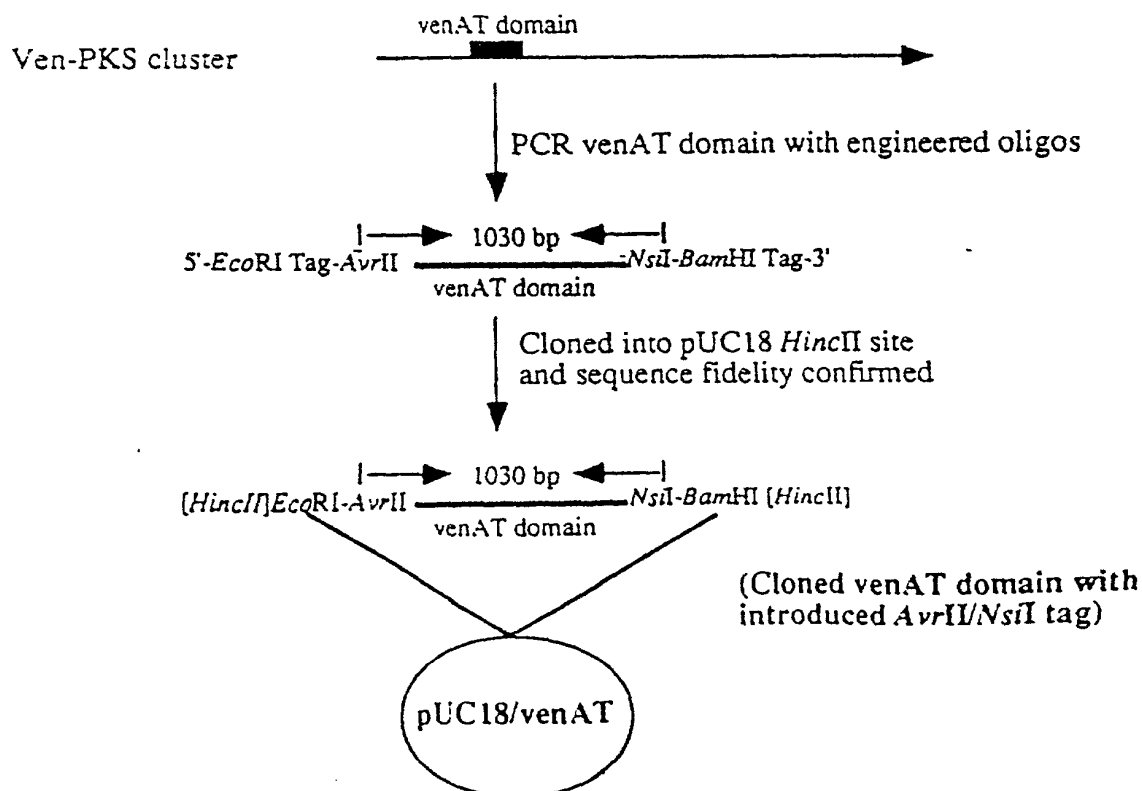


Figure 20

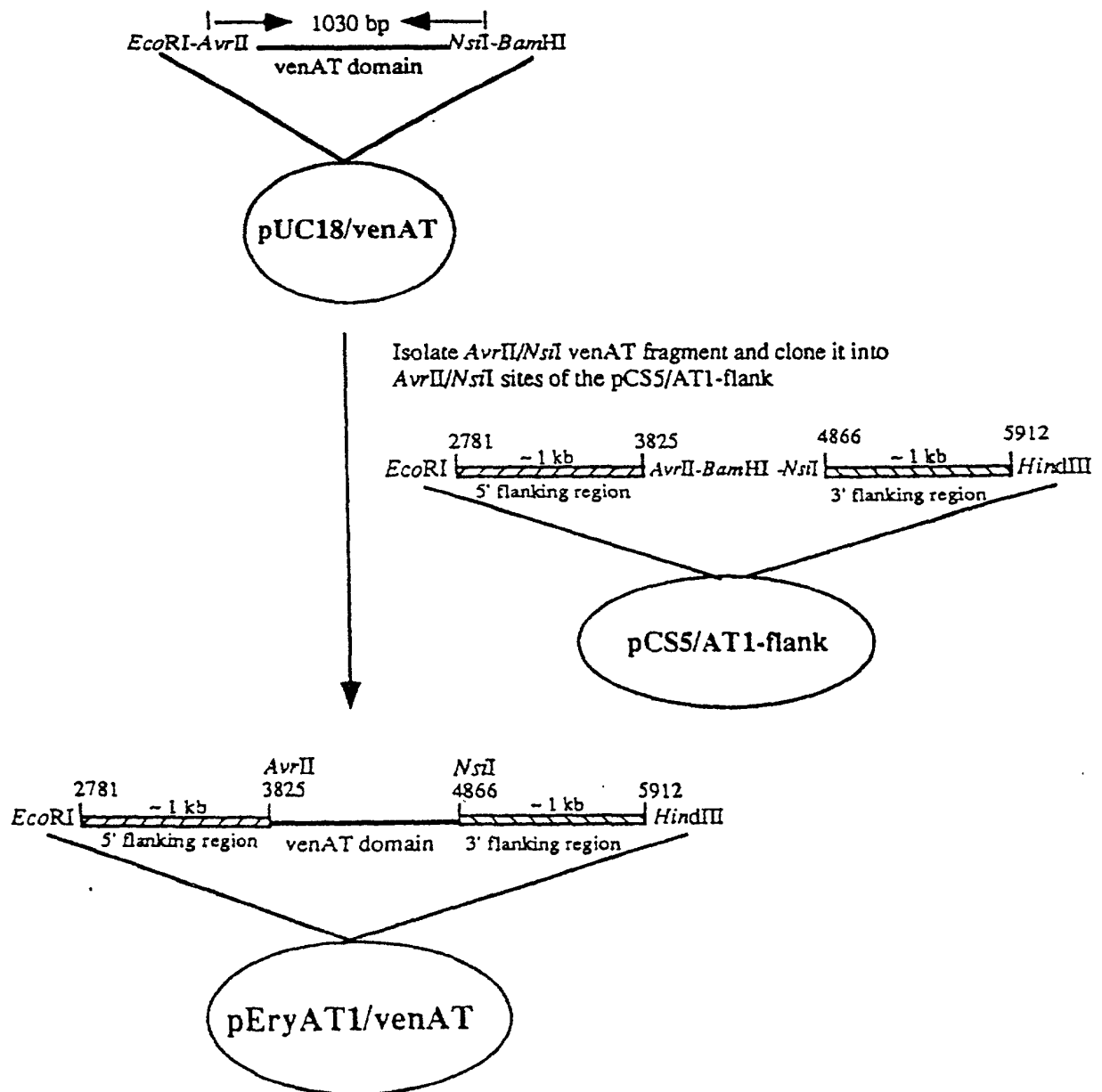
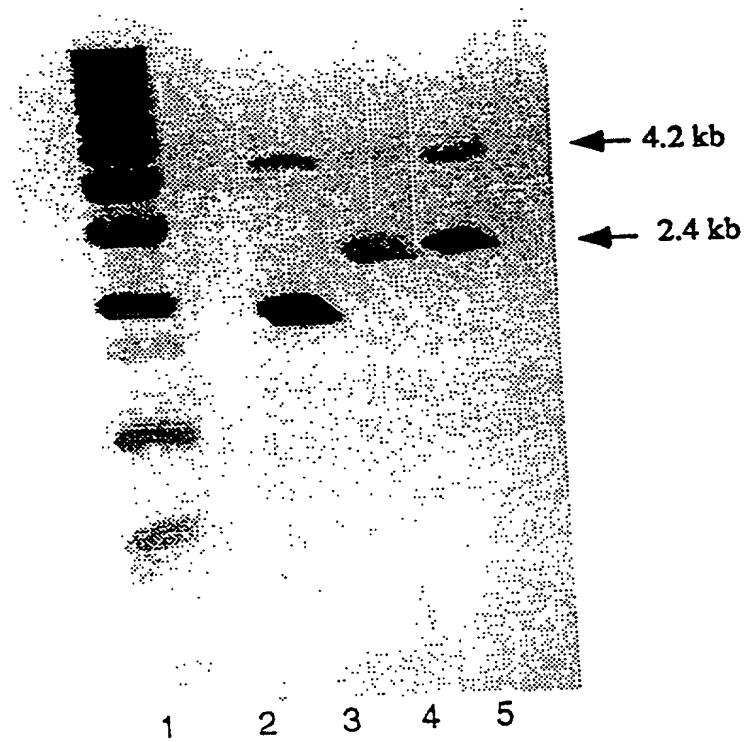
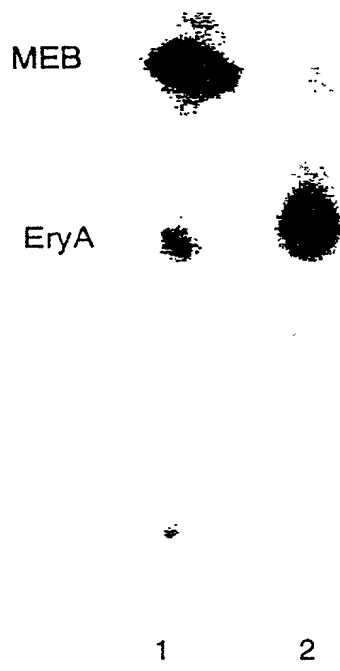


Figure 21



09735056-124100

Figure 22



001111 001111 001111

Figure 23

PCR oligos:

N-terminal Oligo: 5' *EcoRI* Tag-CCTAGGGTTGCCTTCCTGTTTCGAC-3'
 $\overbrace{\text{GGC C}}^{\text{AvrII}}$
 Engineered *AvrII* || Homologous region

C-terminal Oligo: 5' *HindIII* Tag-ATGCATAGACCGGCAGATCCACCG-3'
 $\overbrace{\text{C G}}^{\text{NsiI}}$
 Engineered *NsiI* || Homologous region

PCR cloning:

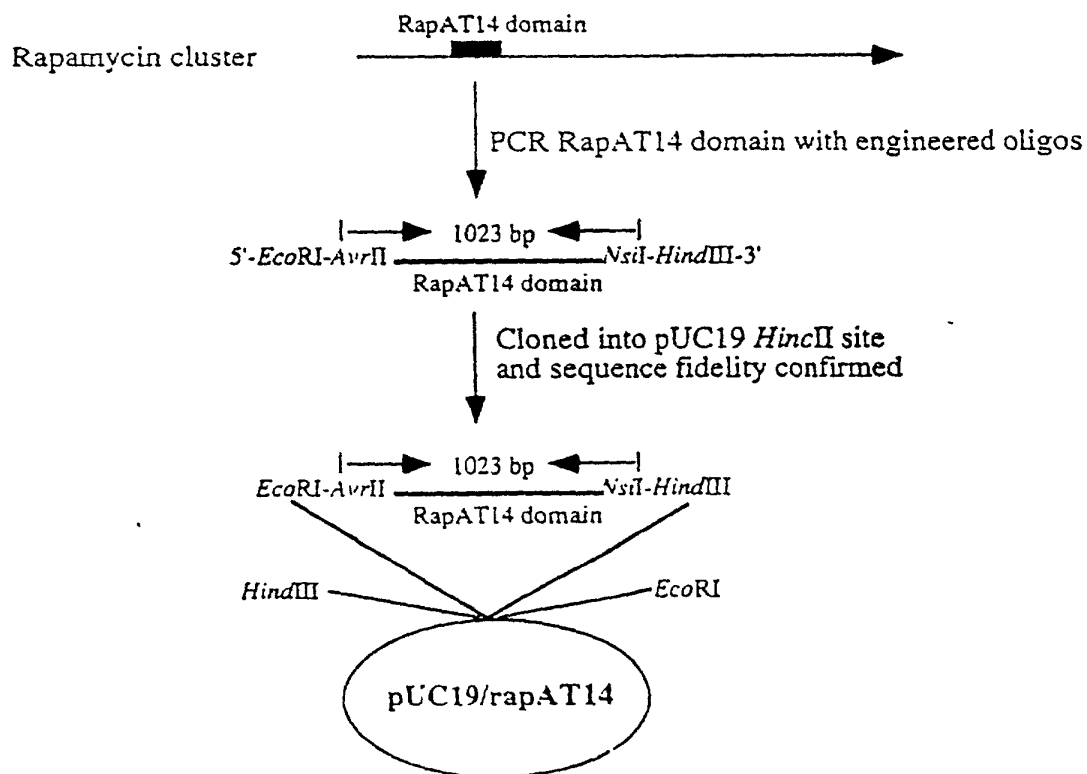
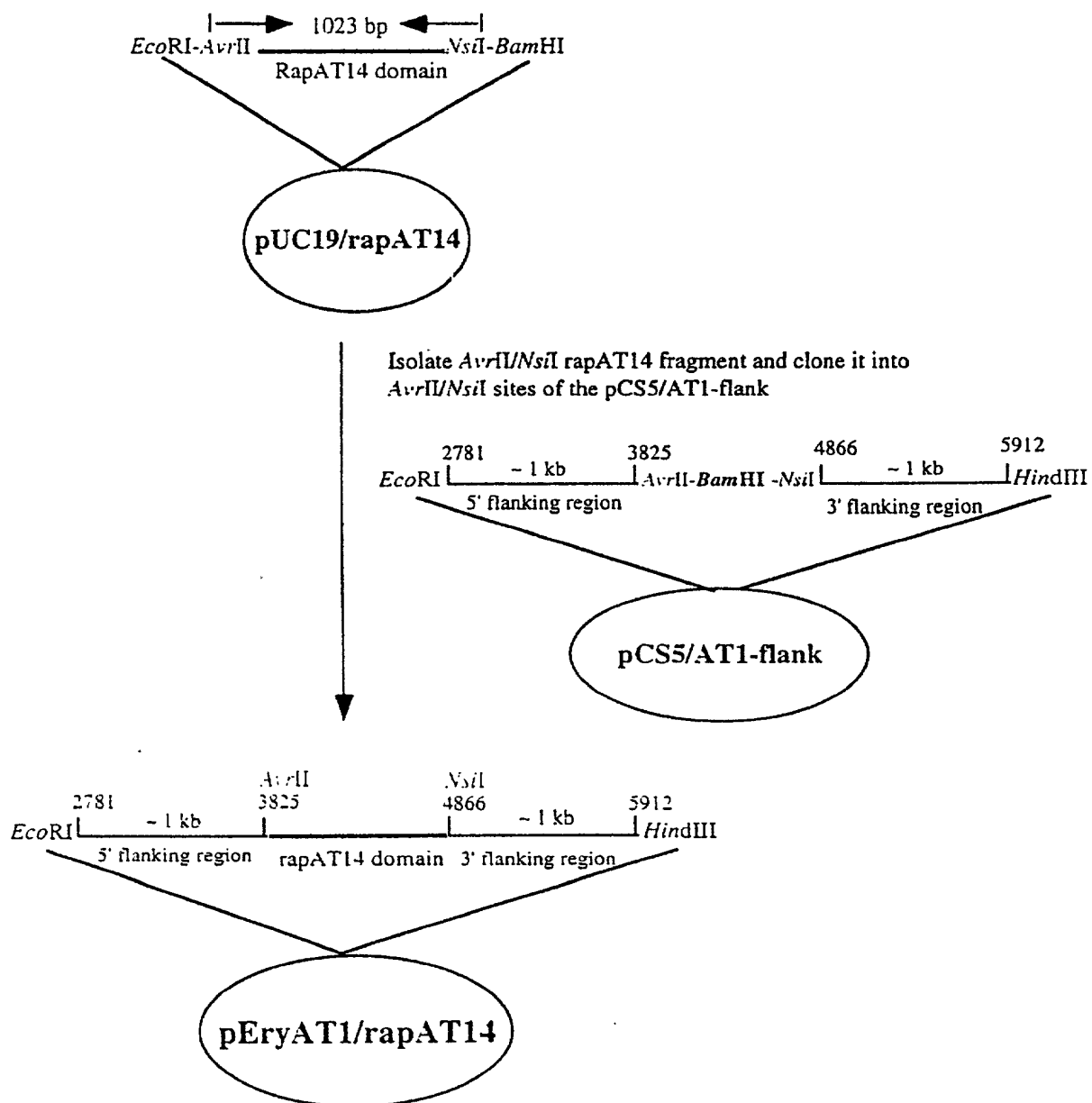
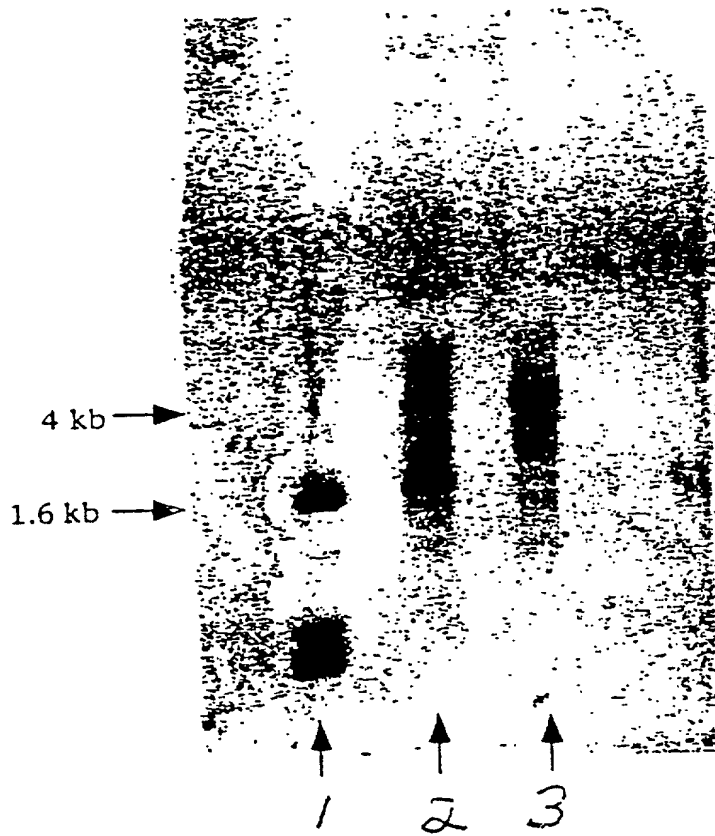


Figure 24



001121 95033/60

Figure 25



001121, 9505E/60

Figure 26



00735056 121100

Figure 27

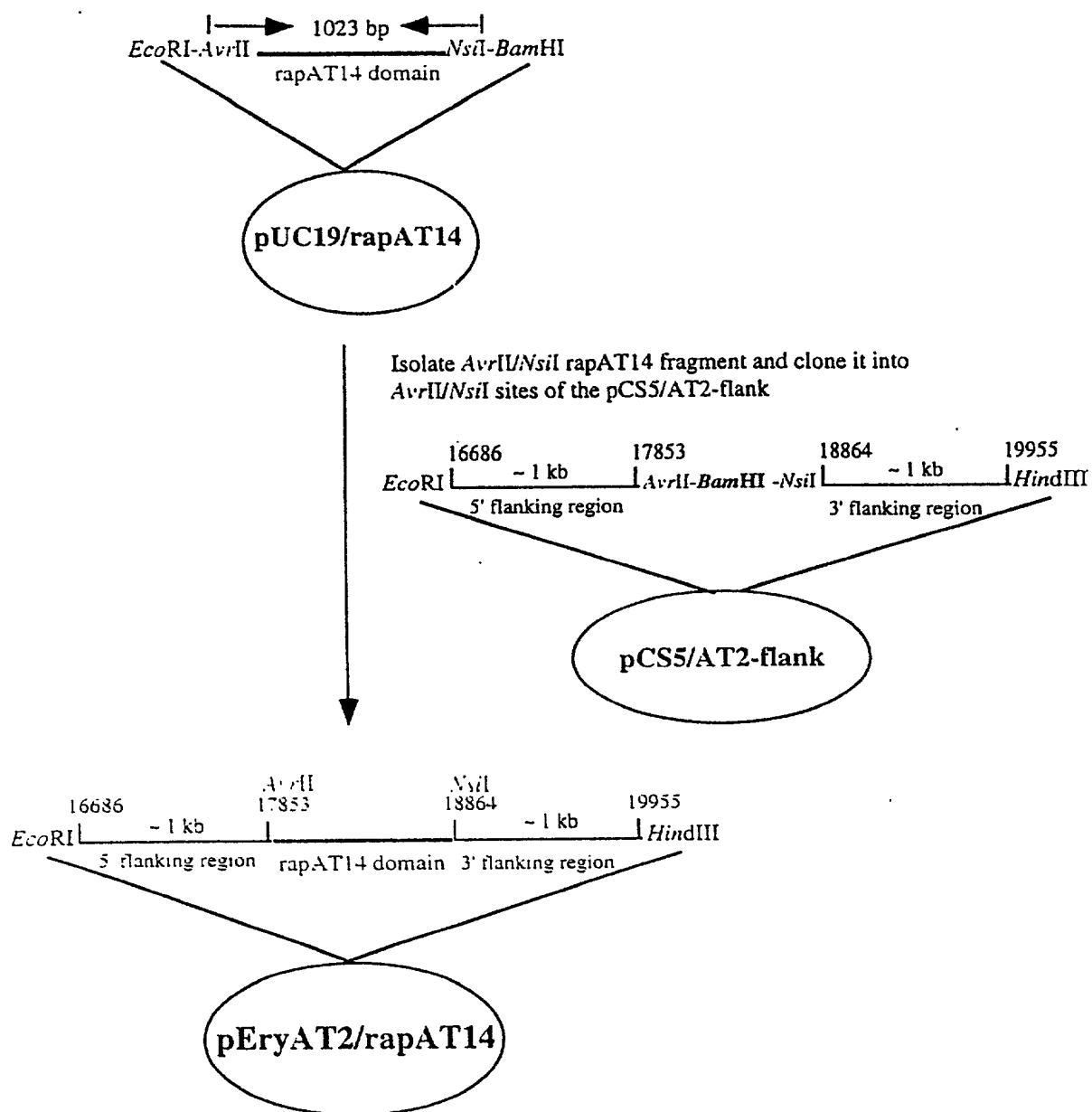
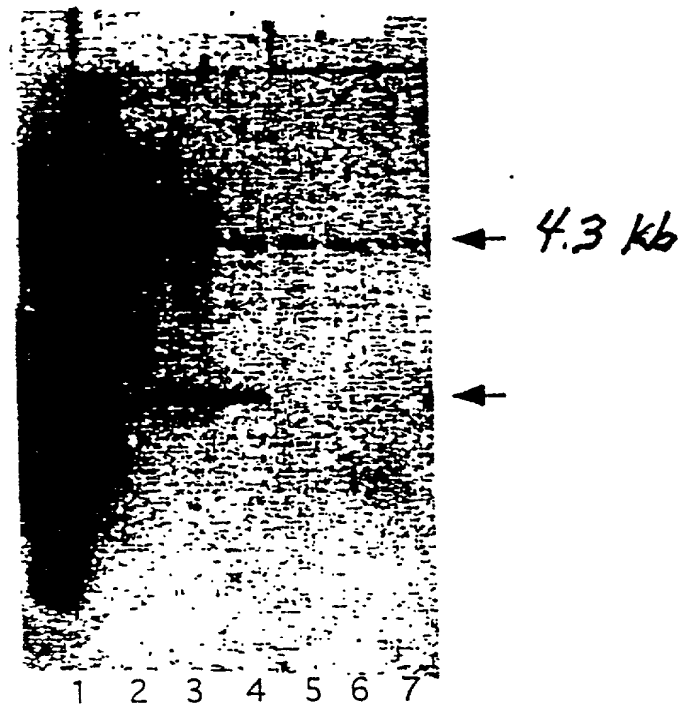
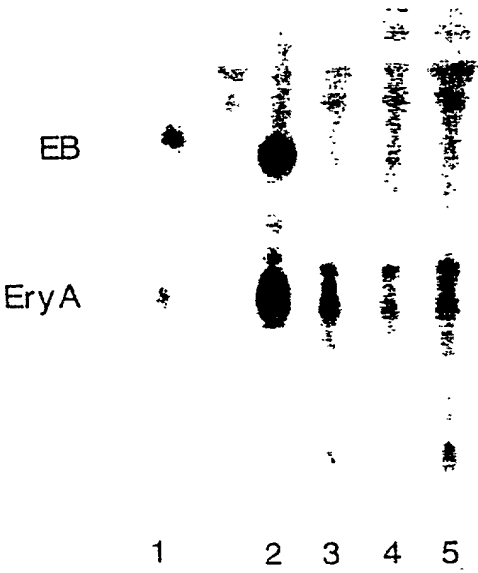


Figure 28



00735056-49400

Figure 29



/

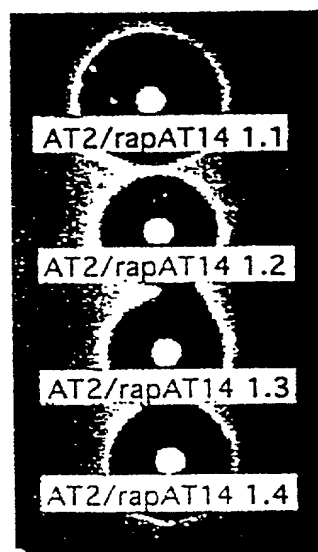


Figure 31

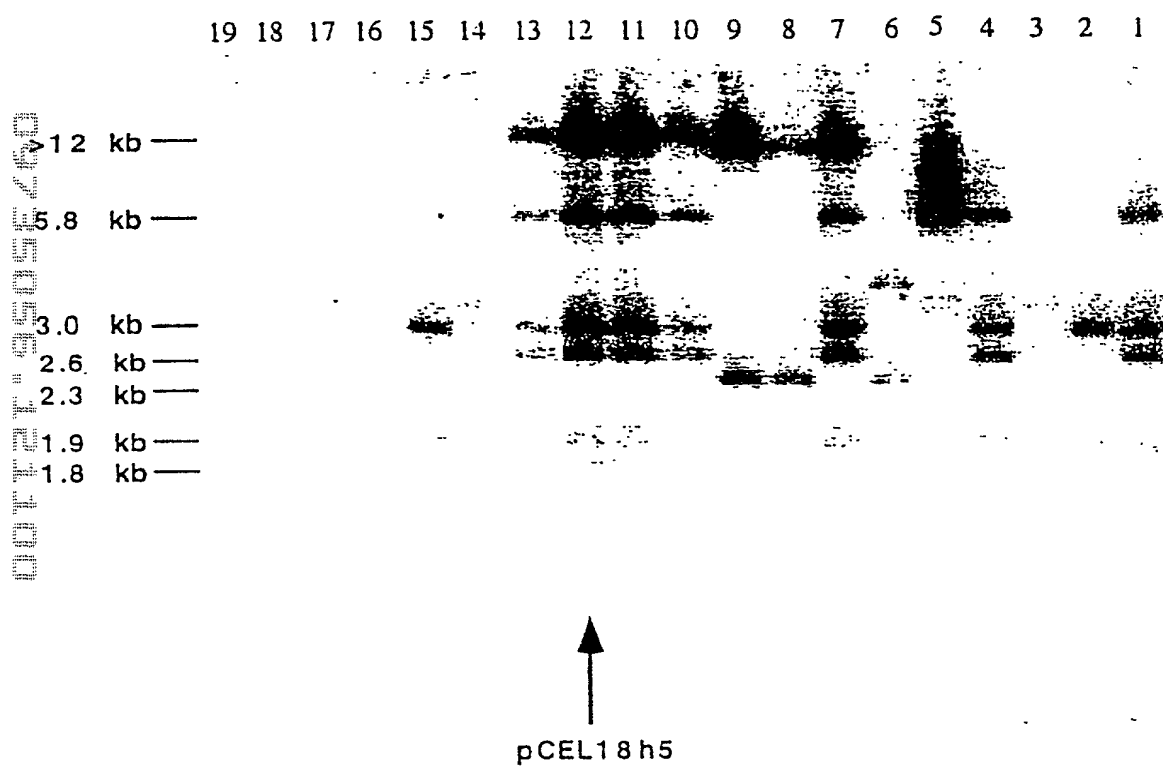
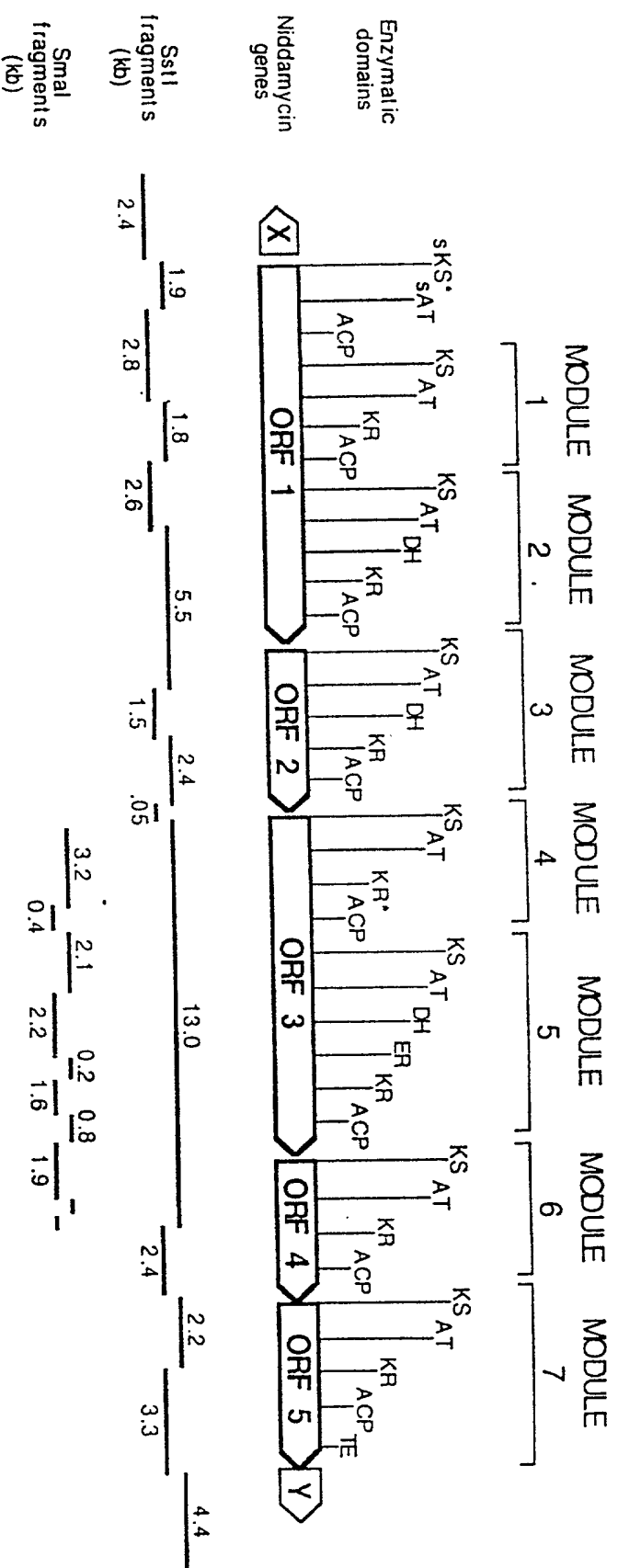


Figure 32



pCEL18h5

pCEL13f5

Variable	Mean	Standard Deviation	Minimum	Maximum
Age	34.5	10.2	21	55
Gender	0.5	0.5	0	1
Marital Status	0.7	0.5	0	1
Education	12.5	1.5	9	16
Income	3500	1500	1000	8000
Health	0.8	0.3	0	1
Stress	4.5	1.5	1	7
Depression	2.5	1.5	0	5
Life Satisfaction	5.5	1.5	1	9
Work Satisfaction	4.5	1.5	1	7
Family Satisfaction	5.5	1.5	1	7
Community Satisfaction	4.5	1.5	1	7
Overall Satisfaction	5.5	1.5	1	7

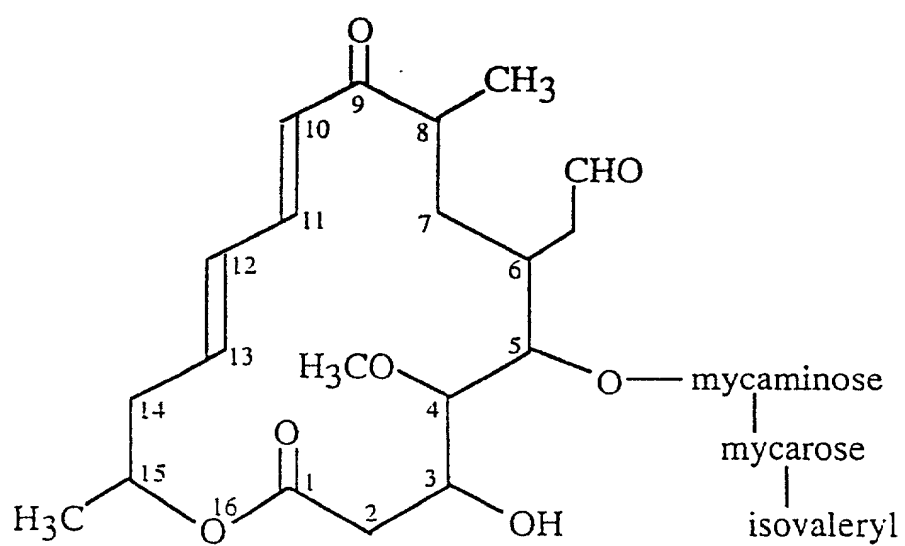


Figure 34

GCCGACCGTGTCTGTTTCGTGTTCCCGGCCAGGGCTCGCAGTGGGCCCGGAATGGCCGAG 60
 A D R Y V F V F P G Q G S Q W A G M A E 20
 GGGCTGCTGGAGCGGTCCGGCGCGTTCGGAGTGC GGCCGACTCGTGCGACGCCGCGCTG 120
 G L L E R S G A F R S A A D S C D A A L 40
 CGGCCGTACCTCGGCTGGTTCGGTGCTGAGCGTGCTGCGCGGGGAACCGGACGCGCCCTCG 180
 R P Y L G W S V L S V L R G E P D A P S 60
 CTCGACCGGGTTCGACGTCTGTCAGCCGGTGCTGTTTCACGATGATGGTCTCGCTCGCGGCG 240
 L D R V D V V Q P V L F T M M V S L A A 80
 GTCTGGCGTGCGCTGGGGGTGGAACCGGCGGCGGTCTCGGGCACTCGCAGGGTGAGATC 300
 V W R A L G V E P A A V V G H S Q G E I 100
 GCCGCTGCCCATGTCTGCCGGTGCGCTGTCTGCTGGACGACTCGGCCCGGATCGTCTGCCCTG 360
 A A A H V A G A L S L D D S A R I V A L 120
 CGCAGTCGGCGTGGCTCGGACTGGCGGGCAAGGGCGGCATGGTGGCGGTGCCGATGCCG 420
 R S R A W L G L A G K G G M V A V P M P 140
 GCGGAGGAGCTGCGGCCGCGGCTGGTGACGTGGGGGGACCGTCTGGCCGTCGCCGCCGTC 480
 A E E L R P R L V T W G D R L A V A A V 160
 AACAGCCCCGGTTCCTGCGCCGTCGCAGGCGACCCCGGAGGCGCTGGCCGAACCTGGTGGCG 540
 N S P G S C A V A G D P E A L A E L V A 180
 CTGCTGACCGGTGAGGGGGTGACGCCCCGGCCGATCCCCGGCGTCTGACACGGCGGGCCAC 600
 L L T G E G V H A R P I P G V D T A G H 200
 TCGCCGCAAGTGGACGCGCTTGCGGGCTCATCTGCTGGAGGTGCTGGCCCCGGTTCGCCCCC 660
 S P Q V D A L R A H L L E V L A P V A P 220
 CGACCGGCCGACATCCCGTTCTACTCGACGGTGACCGGCGGGCTGCTGGACGGCACCGAG 720
 R P A D I P F Y S T V T G G L L D G T E 240
 CTGGACGCGACGTA CTGGTACCGCAACATGCGCGAGCCCGTCTGAGTTCGAGCGGGCCACA 780
 L D A T Y W Y R N M R E P V E F E R A T 260
 CGGGCGCTGATCGCCGACGGGCACGACGTCTTCCTGGAGACGAGCCCGCATCCCATGCTG 840
 R A L I A D G H D V F L E T S P H P M L 280
 GCCGTGGCGCTGGAGCAGACGGTCAACGACGCCGGCACCGACGCGGCGGTGCTCGGGACC 900
 A V A L E Q T V T D A G T D A A V L G T 300
 CTGCGCCGCGGCCACGGCGGTCTCTCGCGCGTGGCCCTGGCCGCTCTGCCGCGCCTTCGCG 960
 L R R R H G G P R A L A L A V C R A F A 320
 CACGGCGTGGAGGTGGACCCCGAGGCGGTCTTCGGTCCGGGCGCACGGCCCGTGGAGTTG 1020
 H G V E V D P E A V F G P G A R P V E L 340
 CCCACCTATCCG 1032
 P T Y P 344

093505C-12100

Figure 35

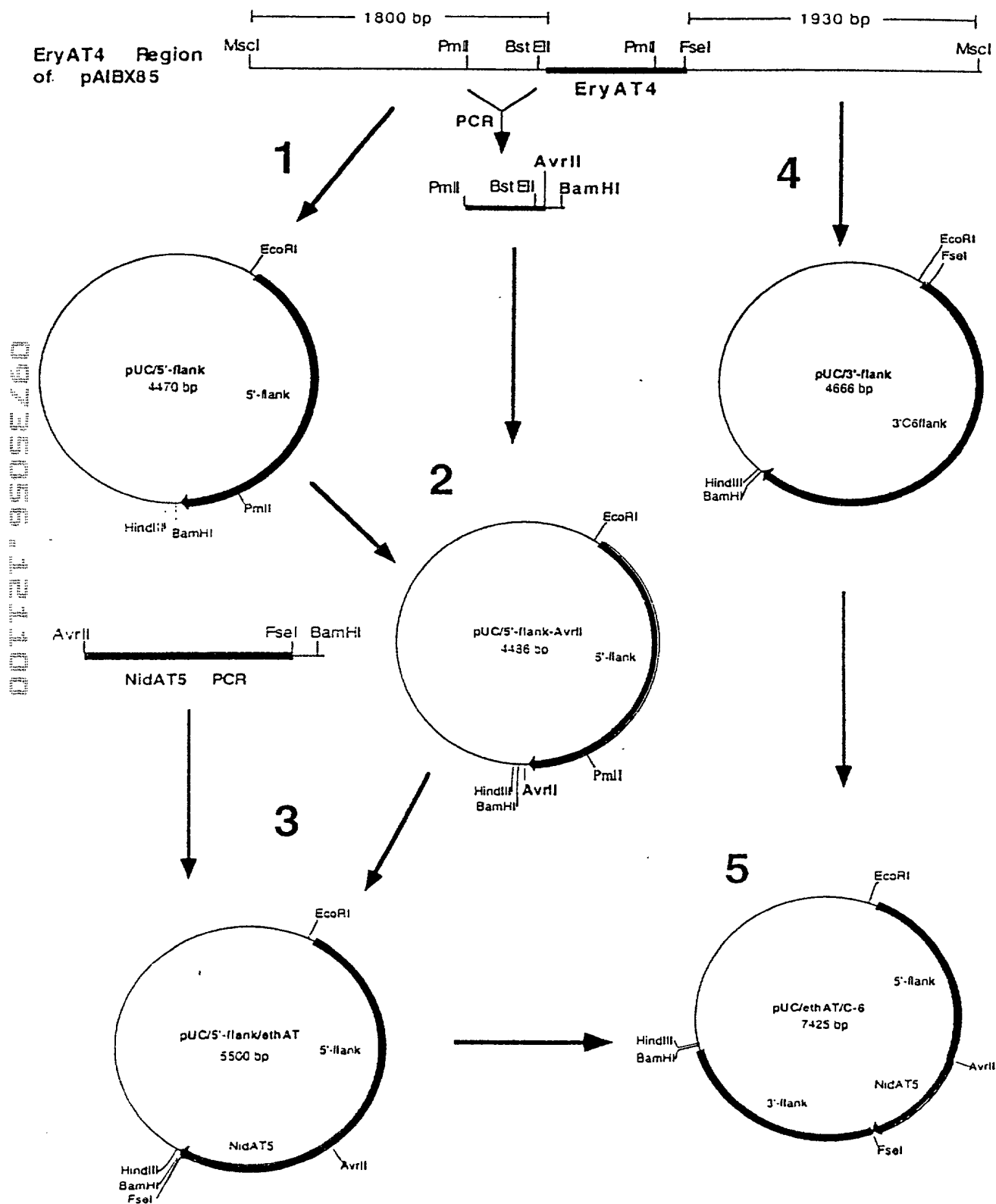


Figure 36

Protein Sequence	S A P R K P
Original Sequence	TCCGCGCCGCGCAAGCCG
Altered Sequence	TCCGCGCCTAGGAAGCCG

PCR Oligos for 5'-flank AvrII site

N-Terminal oligo (Seq 10 no 21) 5'-GAGAGAGGAACCAACGCGCACGTGATCGTCGAAGAGGCACCAGC

C-terminal oligo (Seq 10 no 22) 5'-GAGAGAGGATCCGACCTAGGCGCGGAGGTCAACGGCGCGACGGCG

PCR oligos for NidAT5 fragment

N-Terminal oligo (Seq 10 no 23) 5'-GAGAGACCTAGGAAGCCGGTGTTTCGTGTTCCCCGGCCAGGGCT

C-terminal oligo (Seq 10 no 24) 5'-GAGAGAGGATCCGAGGCCGGCCGTGCGCCCGGACCGAAGACCGCCTC

Figure 37

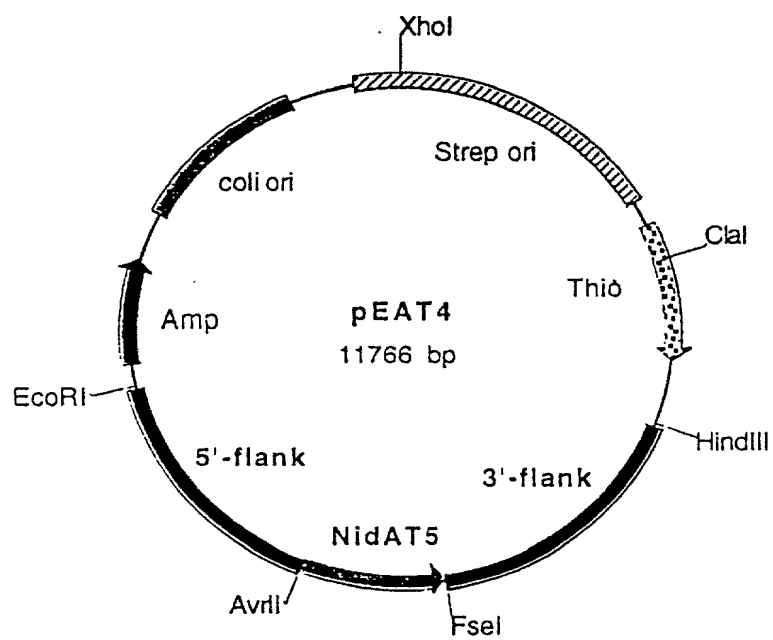
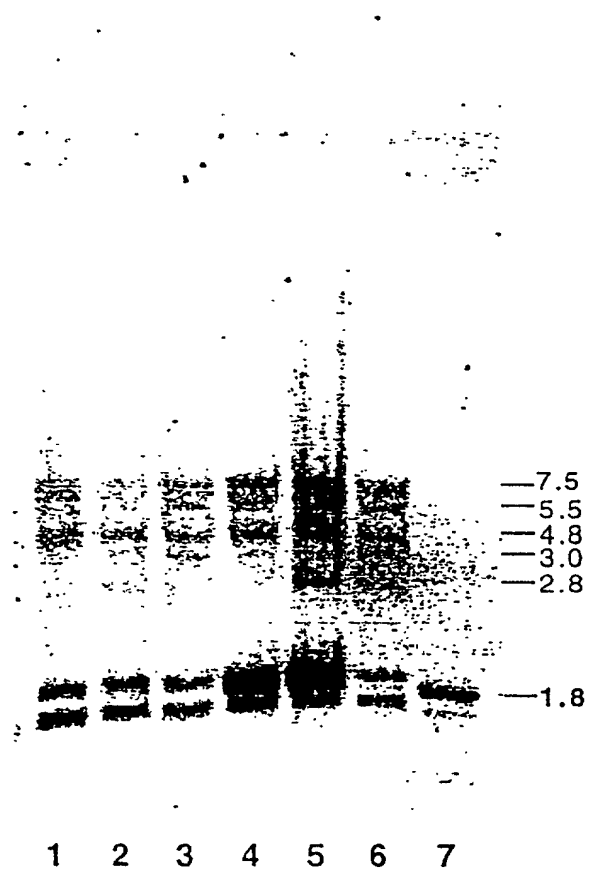
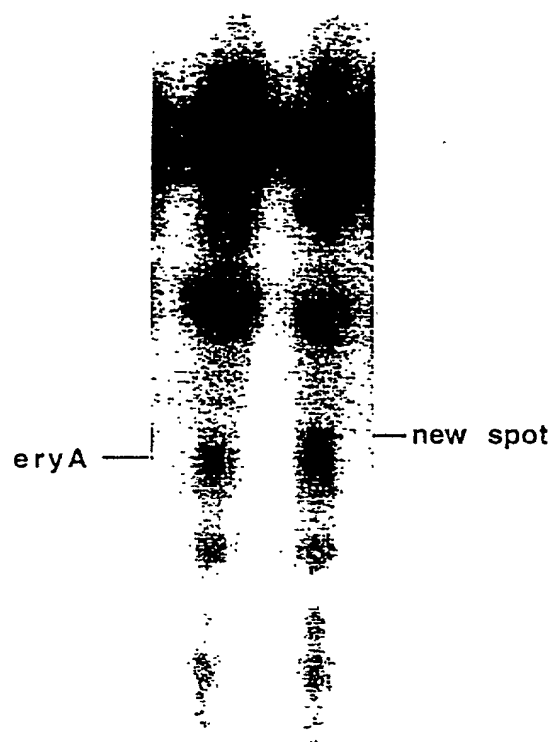


Figure 38



09735056 421100

Figure 39



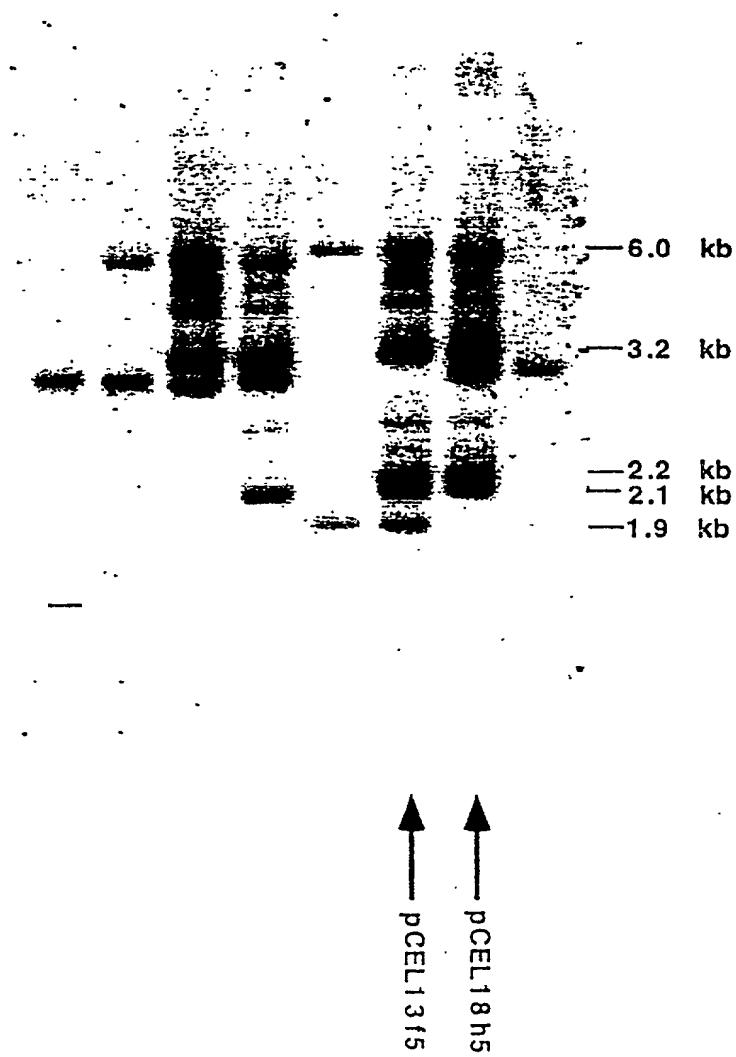
A) SCM only

B) SCM + 50mM butyric acid

A

B

Figure 40



09735056 121100

[illegible]

CGCGCGCCTGCCTTCGTCTTTCCCGGGCAGGGCGCCAGTGGGCGGGACTGGGAGCGCGG 60
R A P A F V F P G Q G A Q W A G L G A R 20

CTCCTCGCGGACTCCCCCGTCTTCCCGGCCAGGGCCGAGGCATGCGCGCGGGCGCTGGAG 120
L L A D S P V F R A R A E A C A R A L E 40

CCTCACCTCGACTGGTTCGCTCGACGTGCTGGCCGGCGCCCCGGGCACCCCTCCCATC 180
P H L D W S V L D V L A G A P G T P P I 60

GACCGGGCCGACGTGGTGCAGCCGGTGCTGTTTACCACGATGGTCTCGCTGGCCGCCCTC 240
D R A D V V Q P V L F T T M V S L A A L 80

TGGGAGGCCCCACGGGGTGGCGCCGGCCGCGGTCTGGGCCACTCCCAGGGCGAGGTGGCC 300
W E A H G V R P A A V V G H S Q G E V A 100

CGCGCCTGCGTGGCCGGTGCCCTGTCGCTGGACGACGCTGCCCTGGTGATCGCCGGACGC 360
A A C V A G A L S L D D A A L V I A G R 120

AGCAGGCTGTGGGGGCGGCTGGCCGGGAACGGCGGGATGCTCGCGGTGATGGCTCCGGCC 420
S R L W G R L A G N G G M L A V M A P A 140

GAGCGGATCCGTGAGCTGCTCGAACCATGGCGGCAGCGGATTTTCGGTGGCGGCGGTCAAT 480
E R I R E L L E P W R Q R I S V A A V N 160

GGCCCCGCTCGGTACCGTCTCCGGTGACGCGCTCGCGCTGGAGGAGTTCGGCGCGCGG 540
G P A S V T V S G D A L A L E E F G A R 180

CTCTCCGCGAGGGGGTGCTGCGCTGGCCGCTGCCGGGCGTCGACTTCGCCGGCCACTCG 600
L S A E G V L R W P L P G V D F A G H S 200

CCGCAGGTGGAGGAGTTCGCGCTGAGCTCCTGGACCTGCTCTCCGGCGTACGGCCGGCT 660
P Q V E E F R A E L L D L L S G V R P A 220

CCTTCGCGGATACCTTTCTTCTCCACCGTGACGGCGGGTCCTTGCGGCGGCGACCAGCTG 720
P S R I P F F S T V T A G P C G G D Q L 240

GACGGGGCGTACTGGTACCGCAACACGCGCAACCCGTGGAGTTCGACGCCACGGTCCGG 780
D G A Y W Y R N T R E P V E F D A T V R 260

GCGCTGCTGCGTGCGGGCCATCACACGTTTCATCGAGGTTCGGTCCGCATCCGCTGCTCAAC 840
A L L R A G H H T F I E V G P H P L L N 280

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A A I D E I A A D E G V A A T A L H T L 300

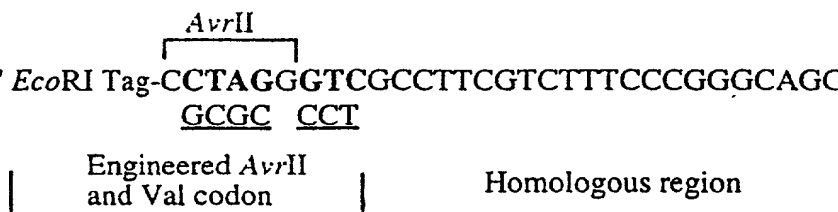
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Q R G A G G L D R V R N A V G A A F A H 320

GGTGTCCGGGTCGACTGGAACGCCCTGTTTCAGGGCACCGGTGCGCGCAGGGTGCCGCTT 1020
G V R V D W N A L F E G T G A R R V P L 340

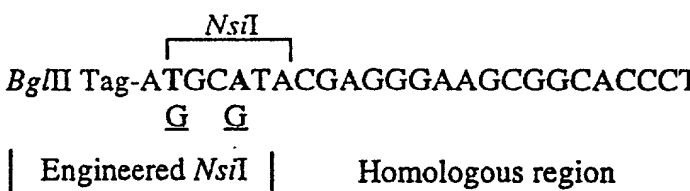
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P S Y A F 345

Table 1. (continued)	
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1.2	0.0000
1.3	0.0000
1.4	0.0000
1.5	0.0000
1.6	0.0000
1.7	0.0000
1.8	0.0000
1.9	0.0000
2.0	0.0000
2.1	0.0000
2.2	0.0000
2.3	0.0000
2.4	0.0000
2.5	0.0000
2.6	0.0000
2.7	0.0000
2.8	0.0000
2.9	0.0000
3.0	0.0000
3.1	0.0000
3.2	0.0000
3.3	0.0000
3.4	0.0000
3.5	0.0000
3.6	0.0000
3.7	0.0000
3.8	0.0000
3.9	0.0000
4.0	0.0000
4.1	0.0000
4.2	0.0000
4.3	0.0000
4.4	0.0000
4.5	0.0000
4.6	0.0000
4.7	0.0000
4.8	0.0000
4.9	0.0000
5.0	0.0000
5.1	0.0000
5.2	0.0000
5.3	0.0000
5.4	0.0000
5.5	0.0000
5.6	0.0000
5.7	0.0000
5.8	0.0000
5.9	0.0000
6.0	0.0000
6.1	0.0000
6.2	0.0000
6.3	0.0000
6.4	0.0000
6.5	0.0000
6.6	0.0000
6.7	0.0000
6.8	0.0000
6.9	0.0000
7.0	0.0000
7.1	0.0000
7.2	0.0000
7.3	0.0000
7.4	0.0000
7.5	0.0000
7.6	0.0000
7.7	0.0000
7.8	0.0000
7.9	0.0000
8.0	0.0000
8.1	0.0000
8.2	0.0000
8.3	0.0000
8.4	0.0000
8.5	0.0000
8.6	0.0000
8.7	0.0000
8.8	0.0000
8.9	0.0000
9.0	0.0000
9.1	0.0000
9.2	0.0000
9.3	0.0000
9.4	0.0000
9.5	0.0000
9.6	0.0000
9.7	0.0000
9.8	0.0000
9.9	0.0000
10.0	0.0000

N-terminal Oligo: 5' *Eco*RI Tag-CCTAGGGTCGCCTTCGTCTTCCCGGGCAAGG-3'
 GCGC CCT



C-terminal Oligo: 5' *Bgl*III Tag-ATGCATACGAGGAAGCGGCACCCTGC-3'



Niddamycin cluster

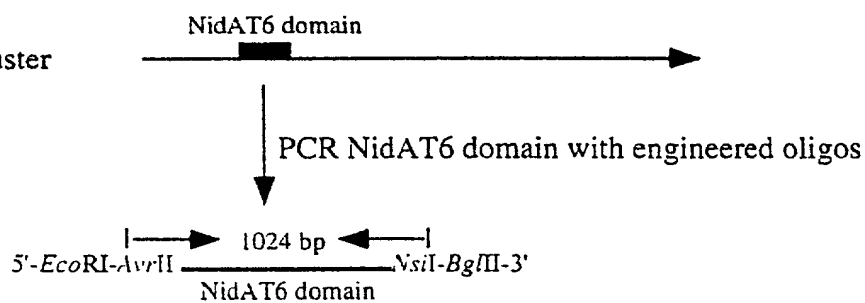
NidAT6 domain

PCR NidAT6 domain with engineered oligos

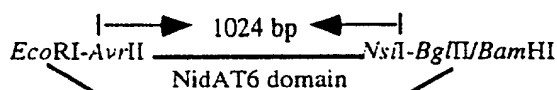
1024 bp

5'-EcoRI-AvrII NsiI-BglII-3'

NidAT6 domain



Cloned into pUC18 *Eco*RI-*Bam*HI sites
and sequence fidelity confirmed



(Cloned NidAT6 domain with introduced *AvrII*/*NsiI* sites)

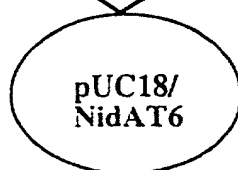
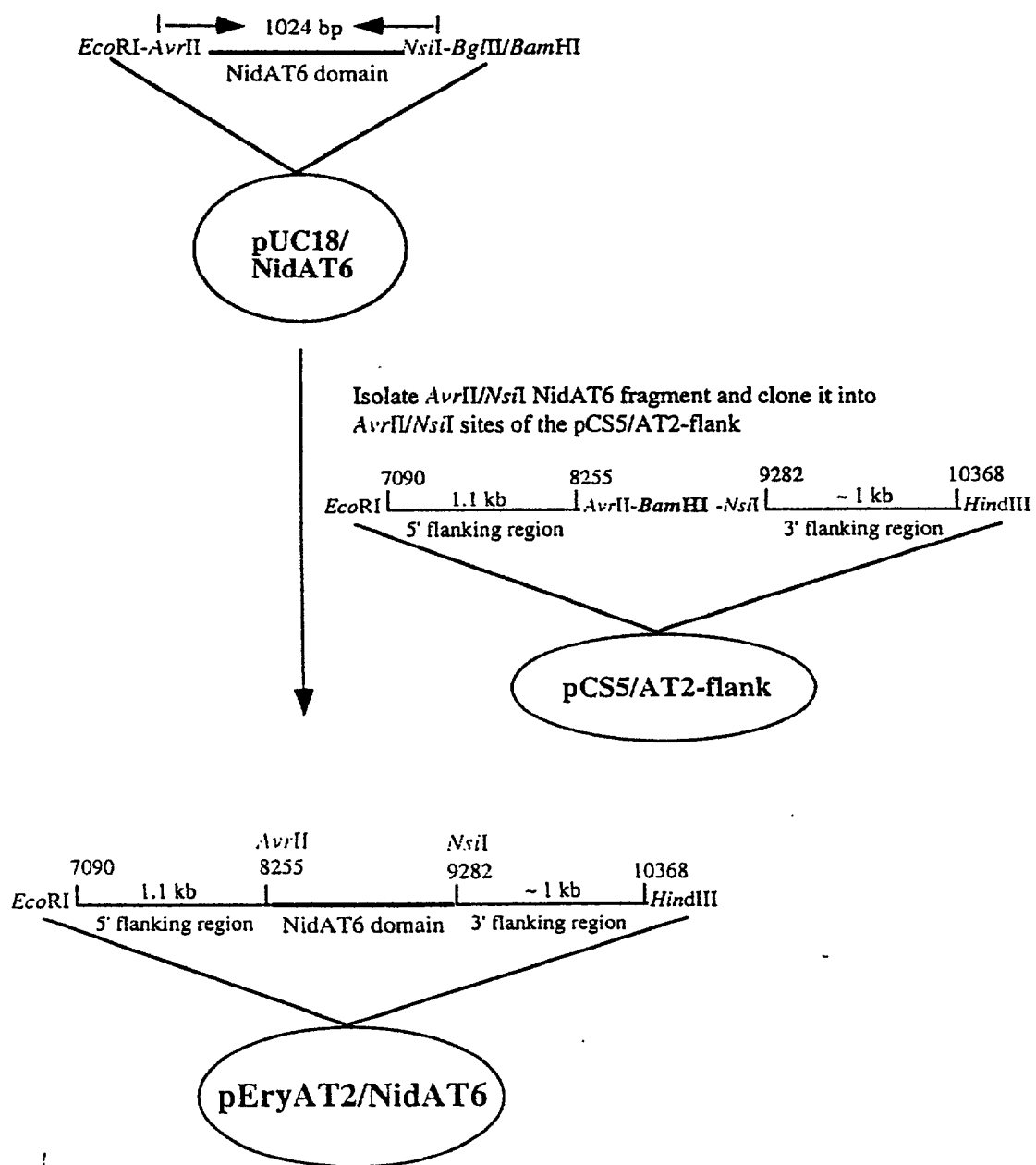


Figure 43



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